376-940

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AC006608 Homo sapt
X59869 Human TCF-1
X59870 Human TCF-1
X59871 Human TCF-1
Z47361 H. sapiens T
Z47361 H. sapiens T
AC04846 Mus muscu
AC05185 Monos emRNA
AC0216756 Homo sapi
AL356157 Human DNA
AC021756 Homo sapi
AC021756 Homo sapi
AC021756 Homo sapi
AC02174 Cow dopamin
AF226537 Cercopith
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Enkaryota, Metazoa: Chordata; Craniata; Vertebrata; Futeleostomi;
Mammalia: Eutheria; Primates: Catarrhin; Hominidae; Homo.
1 (bases 1 to 2855)
                                                                           AC009012 Homo sapi
AC011336 Homo sapi
AC009017 Homo sapi
                                                     x63901 Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   van de Wetering, M., Oosterwegel, M., Holstege, F., Dooyes, D. Suijkerbuijk, R., Geurts van Kessel, A. and Clevers, H. The human T cell transcription factor 1 gene. Structure, Jocalization, and promoter characterization

1. Biol. Chem. 267 (12), 8530-8536 (1992)
              Description
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Van de Wetering,M., Castrop,J., Korinek,V. and Clevers,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I-cell transcription factor; transcription factor
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AC022809
AL137857
AC079140
AC079140
AC079140
AC015525
AC011545
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HSTGFBRIG1
HSB83F04N
S55290
BOVDOPATH
BTPOLAP11
AF226637
HSG6PDGEN
                                                          HSTCF1G
AC009012
AC009017
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HSTCF1B
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99.2 200831

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944444
94471008499499100849910098499910084999
    Result
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                                                                                                                                                             ; Search time 1729.86 Seconds (without alignments) 1153.942 Million cell updates/sec
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1 accagoggcatgtacaaaga.....gctggtaagtggaccccgcc 121
                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                  February 20, 2002, 14:22:05
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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Post-processing:

Database

Minimum DB seq Maximum DB seq

Title: Perfect score: Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

30-SEP-1999

0;

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Consensus quality: 78189 bases at least 040
Consensus quality: 82001 bases at least 030
Consensus quality: 82001 bases at least 030
Consensus quality: 82001 bases at least 030
Consensus quality: 8201 bases at least 030
Consensus quality: 8201 bases at least 030
Consensus quality: 8201 bases at least 030

Estimated insert size: 83944; sum-of-contids estimation
Duality coverage: 6.34 in 020 bases; pulse field qel estimation

* NOTE: This is a 'working draft' sequence. It currently

* romsists of 7 contigs. Gaps between the contigs

* are represented as runs of N. The order of the picres

* to the qaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* the accession number will be preserved.

* the accession number will be preserved.

* 3080

* 34576: contig of 2979 bp in length

* 34577

* 34677

* 59363: 76010: contig of 16648 bp in length

* 59363

* 59363 T6010: contig of 16648 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 14, 2001 this Sequence version replaced gi:7454202.
-----Genome Center
Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                           Homo sapiens chromosome 5 clone XXp1-360D11, WORKING DRAFT SEQUENCE, 7 ordered pieces.
                                                                         l accagoggoatglacaaagagaccglctactccgcctlcaalctgctcatgcattaccca 60
                                          .;
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       Length 2855;
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                            0
         Query Match 100.0%; Score 121; DB ^{\prime\prime}; Best Local Similarity 100.0%; Pred. No. 3.2e-23; Matches 121; Conservative 0; Mismatches 0;
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Center Project Name: 1189075, H71
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: XXp1-360D11
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DOE Joint Genome Institute.
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1691. 1798,1843 .1890,2054 .2134)
//gene="TCF-1"
/codon_start=1
Extensive alternative splicing and dual promoter usage generate TcF-1 protein isoforms with differential transcription control properties
                                                                                               (dases 1 to 2855)
Van de Wetering, M.L.
Direct Submission
Submitted (07-JAN-1992) M.L. Van De Wetering, Department of Immunology, P.O. Box 8550, 3508 GA Utrecht, THE NETHERLANDS Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 others
                                                 Mol. Cell. Biol. 16 (3), 745-752 (1996)
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/db_xref="taxon:9606"
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/cell_type="r-lymphocyte"
/clone="phi-TCF-(5,8.11)"
/map="sq31.1"
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/db_xref="G1:6006565"
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1120 .1209
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/number=4
/1420. 1581
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/gene="TCF-1"
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/gene="TCF-1"
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/gene="TCF-1"
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(Deales) I to 86914)

(Deales) I to 86914)

Dob Joint Genome Institute.

Direct Submitted (06-007-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Jul 18, 2000 this sequence version replaced 91:7710593.

Center: Joint Genome Institute

Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 86914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 82614 bases at least 040
Consensus quality: 85622 bases at least 030
Consensus quality: 86892 bases at least 030
Consensus quality: 86892 bases at least 020
Estimated insert size: 89000; pulse field gel cstimation
Batimated insert size: 86914; sum-of-contigs estimation
Quality coverage: 6.4 in 020 bases; pulse field qel cstimation
Quality coverage: 6.56 in 020 bases; sum-of-contigs estimation
* NOTE: This is a "working draft" sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
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99.2%; Score 120; DB 2; Length 84-
Best Local Similarity 100.0%; Pred. No. 3.5e-23;
Matches 120; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         667 others
11 76110: gap of unknown length
11 79613: contig of $3503 bp in length
14 79713: gap of unknown length
14 80649: contig of 936 bp in length
15 80749: gap of unknown length
16 84544: contig of 3795 bp in length.
17 Location/Qualifiers
                                                                                                                                                                                                                                 /clone="XXp1-360D11"
21740 c 22203 g 20376 t
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Center clone name: CIT-HSPC_250113

    . 84544
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="5"

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AC009017 159420 bp DNA HTG 20-APR-2001
Homo sapiens chromosome 5 clone XXpl-929G6, WORKING DRAFF SEQUENCE,
26 unordered pieces.
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced qi:11178048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi;
Catarrhini; Hominidae; Homo.
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* NOTE: This is a 'working draft' sequence. It currently to consists of 26 contigs. The true order of the pieces is in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 accagoggatgtacaaagagacogtotactocgcottcaatotgctcatgcattaccoa
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 86914: contig of 86914 bp in length.
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-250113"
/clone=lib="calTech human BAC library C"
3 22135 c 22612 g 21422 t
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Unpublished
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Center Code: JGI
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 159420)
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Center clone name: XXp1-929G6
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DOE Joint Genome Institute.
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                  5: gap of unknown length
2: contig of 1537 bp in length
2: gap of unknown length
3: contig of 16248 bp in length
3: gap of unknown length
3: gap of unknown length
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Consensus quality: 174733 bases at least Q40
Consensus quality: 186693 bases at least Q30
Consensus quality: 186693 bases at least Q30
Consensus quality: 196347 bases at least Q30
Estimated insert size: 198031; sum-of-contigs estimation
Quality coverage: 7.77 in Q20 bases; pulse field qel estimation
Quality coverage: 6.47 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a "working draft' sequence. It currently

* consists of 29 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                  ACCO8608 200831 bp DNA HTG 20-APR-2001
Homo sapiens chromosome 5 clone CTB-113120, WORKING DRAFT SEQUENCE,
29 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 Lhis sequence version replaced qi:7708985.
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhiui; Hominidae; Homo.
1 (bases 1 to 200831)
bp in length
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Center clone name: C1T978SKB_113120
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AC008608.5 GI:13699394
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FMLymksmpakvtpactijkesaalnollgrphhalspredomkyvelarkerglihmolv
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van de Wetering,M.
Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht, The Netherlands
2. (bases I to 1254)
van de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H. Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box EMBO J. 10 (1), 123-132 (1991)
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Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical
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DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene
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/protein_id="CAA42526.1"
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                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=experimental
                                                                                                                                                                                                               Location/Qualifiers
1. .1254
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/gene="TCF-1"
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Human TCF-1 mRNA for T cell factor 1 (splice form A).
X59869 X55327
X59869.1 G1:36785
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101550: contig of 20504 bp in length
101750: gap of unknown length
137108: contig of 35358 bp in length
137208: gap of unknown length
200831: contig of 63623 bp in length.
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gap of unknown length
contig of 14900 bp in length
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contig of 7268 bp in length
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/clone_lib="cDNA"
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LSLYERVRSPHPTPARADISOKOWHPRIOTPDISGFYSLYGSGWOLDHPTSWFTHPS
LMLGSGVBGHPARADIPPSGKOBLOPPDRNIKTOAESKAREAKKFTIKKPLNK
PMLYMKBMARVIAECTIKESAAINQIIGRRWHALSREEOAKYYELARKEROLHWOLY
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Catarrhini, Hominidae, Homo.
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Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical
Immunology, University Hospital, P.O. Box 85500, 3508 GA Ulrecht,
The Netherlands
     University Hospital, P.O. Box 85500, 3508 GA Utrecht,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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2 (bases 1.0. 2814)

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3 (bases 1.0. 2814)

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5 (bases 1.0. 2814)

6 (costerwegel, M., Dooijes, D. and Clevers, H.

7 (costering, M., Oosterwegel, M., oosterwegel, M., oostering, Bentification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box EMBO J. 10 (1), 123-132 (1991)

8 (costering M.)

8 (costering M.)

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Human TCF-1 mRNA for T cell factor 1 (splice form C).
X59871 X55328
X58871.1 GT:36789
DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="T cell factor 1 splice
/protein_id="CAA42527.1"
/db_xref="G1:36788"
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100.0%; Pred. No. 7.6e-19;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T lymphocyte"
/cell_line="Jurkat and HPB-ALL"
/clone_lib="cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="alternative splice site"
831 c 648 g 572 t
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Manmalla, Eutheria; Primates;
1 (bases 1 to 2910)
van de Wetering, M.
                                                                                                                                                                                                                                            Location/Qualifiers
1. .2814
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80. .889
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Eukaryota: Metazoa; Chordata; Craniala; Vertebrata; Buteleoslomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 1115)

Mayer, K., Wolff E.; Clevers, H. and Ballhansen, W.G.
The human high mobility group (HMG)-box transcription factor TCF-1:
novel isoforms due to alternative splicing and usage of a new exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MYKETVYSAFNILMHYPPPSGAGQHPQPQPPLHKANQPPHGVPO"
LSLYEHFNSPHPTPAPADISOKQVHRPLQTPDLSGFYSLTSGSMGQLPPHYSWFTHPS
LLMGSGVPGHPATIPHTPAPADISOKQVHRPLQTPDLSGFYSLTSGSMGQLPHYSWFTHPS
LMGSGVPGHPATIPHTYPPSGKGGLOPPPDRNATTVGTOKRFTIKKPLNA
PMGSRYPERAKVIAFTLKESATIOJILGKRWHALISREEQAKYFIANKFRQIHMQIY
PGWSARDNYGKKRRSFEKHQESTTDPGSPFKCRARPGI.NOGTDWCGPCR"
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rm D.
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van de Wetering,M., Oosterwegel,M., Dooijes,D. and Clevers,H. Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box BMBO J. 10 (1), 123-132 (1991) see also X59869-X59871.
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van de Wetering,M., Oosterwegel,M., Holstege,F., Dooyes,D.,
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H.sapiens TCF-1 mRNA for T cell factor 1 splice form 247361
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1. 2910
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860 c 671 g 597 t
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splice form D; T cell factor 1.
human.
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/gene="TCF-1"
2. .1144
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Ballhausen, W.G.
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Matches 97; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1165)
Mayer, K., Wolff, E., Clevers, H. and Ballhausen, W.C.
The human high mobility group (HMG)-box transcription factor TCF-1:
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LSLYEHFNSPHPTPAPADISOKQVHRPLOTPPDLSGFYSLTSGSMGOLPHTVSWFTHPS
LIMIGSGYCOHPAALPHPATVPPSGAGOELOPPDRNIKTOAFSKAEKEAKKPTIKRPLNA
FMILWKENKRAKTAACTIKESAAINOILGRRWHALSREEGAKYYELARKERQCHMOLY
PGWSARDHYGKKKRRSREHQESTTDNSLHYS"
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Submitted (6-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachhanlage 10, Erlangen, Germany, D-91054
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/function="high mobility group box transcription
Suijkerbuijk,R., Geurts van Kessel,A. and Clevers,H.
The human T cell transcription factor-1 gene. Structure,
localization, and promoter characterization
J. Biol. Chem. 267 (12), 8530-8536 (1992)
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/yeroduct="alternative ORF specific for TCF-1D"
/product="alternative ORF specific for TCF-1D"
/product="alternative ORF specific for TCF-1D"
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/db_xref="G1:619882"
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1. 1115
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2. .754
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/gene="TCF-1"
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Ballhausen, W.G.
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/product="1" cell factor 1 splice form E"
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/db_xref=
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AC044846.
novel isoforms due to alternative splicing and usage of a new exon
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/function="high mobility group box transcription factor"
/evidence=experimental
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van de Wetering,M., Oosterwegel,M., Holstege,F., Dooyes,D.
suijkerbuijk,R., Geurts van Kessel,A. and Clevers,H.
The human T cell transcription factor-1 gene. Structure,
Jucalization, and promoter characterization
J. Biol. Chem. 267 (12), 8530-8536 (1992)
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1824: config of 4205 bp in length 1830 23129: contig of 4205 bp in length 25 23129: contig of 4205 bp in length 30 2329: gap of 100 bp 26859: contig of 3630 bp in length 60 26959: gap of 100 bp 60 32575: contig of 5616 bp in length 63 3275: contig of 5616 bp in length 63 38781: contig of 6106 bp in length 63 38781: contig of 6106 bp in length 63 38781: contig of 6106 bp in length
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140244 140343; gap of 100 bp
140344 162496; contig of 22153 bp in length.
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75189 75288: gap of 100 bp
75289 85641: contig of 10353 bp in length
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109673 122441: contig of 12769 bp in length
122442 12541: gap of 100 bp
122542 140243: contig of 17702 bp in length
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                                   9512: gap of 100 bp 10790: contig of 1278 bp in length 10890: gap of 100 bp 15800: contig of 4190 bp in length 15180: gap of 100 bp 18824: contig of 33644 bp in length
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44764: contig of 5883 bp in length
44864: gap of 100 bp
52115: contig of 7251 bp in length
100 bp
of 2895 bp in length
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clone_end:SP6
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/db_xref="taxon:10090"
/chromosome="ll"
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10891. .15080
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109572: cont
   6517: gap of
9412: cor
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 162496)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 164000; agarose-fp
Insert size: 160296; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: 46_J_7

Center clone name: 46_J_7

Sequencing vector: M13: M77815; 1008 of reads
Chemistry: Dye-terminator B19 Dye; 1008 of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 149639 bases at least Q40

Consensus quality: 158986 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rigap of 100 bp
2786: contig of 1313 bp in length
is gap of 100 bp
4262: contig of 1376 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1373; contig of 1373 bp in length
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                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 11, clone RP23-46J7 Unpublished 2 (bases 1 to 162496)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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             HTGS_PHASE1; HTGS_DRAFT
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6417:
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1474 2786:
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4263 4362:
4363 64
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                                                   Mus musculus
                                 ponse monse
                                                 ORGANISM
                                                                                                    REFERENCE
AUTHORS
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REFERENCE
AUTHORS
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JOURNAL
           KEYWORDS
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COMMENT

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/clone_lib="lambda Zap cDNA"
1. 1790
190. 1101
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AC022646.3 GI:7249102
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                      436 g
                                                                                                                                                                                                                                                                                      761. .984
/note="HMG-box"
                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                   72.7%;
milarity 83.3%;
Conservative 0
                                      .1101
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Matches 100;
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AC022646
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases I to 1790)
Oosterwegel,M., van de Wetering,M., Dooijes,D., Klomp,L.,
Wincto,A., Georgopoulos,K., Meijlink,F. and Clevers,H.
Cloning of murine TCF-1, a T cell-specific transcription factor
interacting with functional motifs in the CD3-epsilon and T cell
receptor alpha enhancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol,
THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 61983 CGGCCTCCGGAGCAGCAGCATCCGCAGCCTCAACCCCCGCTGGTAAGTGACCGAAGC 61925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMG box; T-cell specific transcription factor; transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Clin In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 162496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse mRNA for T-cell specific transcription factor.
X61385
                                                                                                                                                                                                                                                                                                                                                                                           2206 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-AUG-1991) M.A. Oosterwegel, Dept
Univ Hospital Utrecht, P.O. Box 85500, 3508 GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 91.8; DB 2;
Pred, No. 1.6e-15;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                          sature 140344. .162496
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42470 a 37212 c 36404 g 44204 t
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91217625
                                                         7.016- G35927

7.0016- "assembly_fragment"

6.0028 " . 67115

7.0046- "assembly_fragment"

6.0216 . . 75188

7.016- "assembly_fragment"

75289 . . 85641

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7.016- "assembly_fragment"
                                                                                                                                                                                                                                                            109673. 122441
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                             14865. .52115
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                             122542. .140243
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                            vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.9%;
Best Local Similarity 85.7%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                              clone_end:T7
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Oosterwegel, M.A.
Direct Submission
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LOCUS
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unpublished
Updaes I to 16653)

Birren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Baduslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., Fitzludy, W., Forrest, C., Gaqe, D., Galagan, J.,
Farreira, P., Fitzludy, W., Forrest, C., Gaqe, D.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McKeman, P., McGurk, A., McKernan, K.,
McPheelers, R., Mardim, N., Menens, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Pierre, N., Pistani, C., Pollara, V., Raymond, C., Rlley, K., Rothman, D.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfuye, S., Theodore, J.,
Tirrell, A., Wassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
Zimmer, A. and Zody, M.
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/db_xref="MGD:86198607"
/db_xref="WGD:86198607"
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Homo sapiens clone RP11-28C18, WORKING DRAFT SEQUENCE, 18 unordered
pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidac; Homo.
1 (bases 1 to 166523)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-28C18
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Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 3.6e-14;
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761. .984
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AL356157 198917 bp DNA PRI 03-JUL-2001
Human DNA sequence from clone RPII-733D4 on chromosome 10, complete
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Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (03-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 31974 AACCTCCTGCAGCTTGGTGCCTGCCCAAACAGCTGCTGTTTGTCCTTGAAACCG 32031
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Live 0; Mismatches 52; Indels 0;
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49468 a 32573 c 33029 g 49750 t
                                                                                                                                                                                                  /note="assembly_fragment"
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116278. .134153
/note="assembly_fragment"
          1. .1099
/note="assembly_fragment"
1200. .2705
                                                                                        2806. .4225
/note="assembly_fragment"
4326. .5737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84224. .100094 // note="assembly_fragment"
                                                                /note="assembly_fragment"
                                                                                                                                            /note="assembly_fragment"
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/note="assembly_fragment
clone_end:SP6
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Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
1 (bases 1 to 198917)
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70265. .84123
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AL356157.14 GI:14596303
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Best Local Similarity 55.99
Matches 66, Conservative
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AL356157/c
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ORGANISM
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JOURNAL
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KEYWORDS
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                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                            Center clone name: 28_C_18
Sequencing vector: M13; M77815; 108 of reads
Sequencing vector: M13; M77815; 108 of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 157134 bases at least Q40
Consensus quality: 161890 bases at least Q30
Consensus quality: 163469 bases at least Q30
Insert size: 156000; agarose-fp
Insert size: 164823; sum-of-contigs
Quality coverage: 5.2 in Q20 bases; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is
On Mar 16, 2000 this sequence version replaced yi:6984422 All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                   100 1199: contig of 1099 bp in length 1100 1199: gap of 100 bp 1200 2705: contig of 1506 bp in length 2806 4225: contig of 1420 bp in length 4226 4325: gap of 100 bp 1426 4325: gap of 100 bp 5738 5837: contig of 1412 bp in length 5738 5837: gap of 100 bp 5838 7280: contig of 1443 bp in length
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84224 100094: contig of 15871 bp in length
100095 100194: gap of 100 bp
116178 116277: contig of 15883 bp in length
116278 134153: contig of 17876 bp in length
114154 13453: gap of 100 bp
114154 14553: contig of 32270 bp in length.
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4 166523: contig of 32270 bp in length.
Location/Qualifiers
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58185: contig of 11492 bp in length
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/clone_lib="RPCI-11 Human Male
                                                                                                                                      Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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/db_xref="taxon:9606"
                                                                                              - Genome Center
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27816 33432: cont
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27715: con
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7381 11595
11596 11695: g
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                COMMENT
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25899. .25948

Arote="MIJID repeat: matches 55. .99 of consensus"
26064. .26105

Anote="All copies 2 mer aa 76% conserved"
Anote="MIJID repeat: matches 353. .429 of consensus"
Anote="MIJID repeat: matches 2. .139 of consensus"
Anote="MIJIM repeat: matches 4529. .5009 of consensus"
Anote="MIJIM repeat: matches 4529. .5009 of consensus"
Anote="MIJID repeat: matches 48. .99 of consensus"
Anote="MIJID repeat: matches 48. .99 of consensus"
Anote="MIJIM repeat: matches 5913. .6401 of consensus"
Anote="MIJIM repeat: matches 5913. .6401 of consensus"
Anote="MIJIM repeat: matches 5913. .6401 of consensus"
Anote="LIPA10 repeat: matches 5767. .6159 of consensus"
Anote: matches 5767. .6159 of consensus"
Anote="LIPA10 repeat: matches 5767. .6159 of consensus"
                                                                                                                                                                                                                                          //note="MIR repeat: matches 29. .135 of consensus"
20669. .20770
//note="MIR repeat: matches 47. .152 of consensus"
20958. .22168
//note="LiP repeat: matches 3882. .5092 of consensus"
22177. .23069
//note="LiP repeat: matches 5254. .6146 of consensus"
20377. .23069
//note="20 copies 2 mer aa 80% conserved"
23171. .23358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //octe="LIM" repeat: matches 5492. .5781 of consensus"
//octe="LIM" repeat: matches 35. .294 of consensus"
35017. .33281
/note="AluY repeat: matches 3825. .5493 of consensus"
36938. .38320
/note="LIM" repeat: matches 6389. .7735 of consensus"
39478. .39323
/note="LIM" repeat: matches 6389. .7735 of consensus"
39478. .39323
/note="MERSB repeat: matches 96. .148 of consensus"
39556. .39872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2075, .2216 of consensus" 44118. .44845 /note="L1MB3 repeat: matches 5447. .6182 of consensus" 45984. .46490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23431. 25705
//octe="LiM4 repeat: matches 2215. .4526 of consensus"
//octe="WRRIB repeat: matches 141. .337 of consensus"
//octe="WRRIB repeat: matches 141. .337 of consensus"
25899. .25948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ### ropeat: matches 2275. .2185 of consensus" 23364. .23429
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   "L2 repeat: matches 1158. .1237 of consensus"
.17666
                                                                        ,2696 of consensus"
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40558. .40687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 24. .233 of consensus"
41306. .41596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .281 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluJ/FRAM repeat: matches 216.
                                                                     //note="12 repeat: matches 2169. .2
18929. .18970
/note="21 copies 2 mer ac 100% con
19952. .20346
/note="match: GSS: Em:AQ384380"
20206. .20305
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42492. .42997
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41054. .41249
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                                                                                                                                                                                 misc_feature
CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonereques(@sanger.ac.uk on Jul 4, 2001 this sequence version replaced gi:14329554.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations where differences are found these are annotated as variations together with a note of the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate regions were either double-stranded or sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone: and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at the formation can be found at the constructed by the Sanger Centre Chromosome 10 constructed by the Sanger Centre Chromosome 10 http://www.sanger.ac.uk/HGPC/Chr10 RPII-733D4 is from the library RPCI-11.3 constructed by the group of Plater de Jong. Prof. Information can be found at http://www.chori.org/Daces/Ornio.htm.
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14608. 14681
/note="LiPB1 repeat: matches -485. .-412 of consensus"
14732. .14930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the entire insert of clone RPI1-733D4 The true left end of clone RPI1-523E20 is at 189958 in this sequence. The true right end of clone RPI1-256K7 is at 98701 in this sequence. The true right end of clone RPI3-37403 is at 128227 in this
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/note="LiPB1 repeat: matches 4101. .6155 of consensus"

/note="MER9 repeat: matches 1. .511 of consensus"

11065. 11767

/note="LiPB1 repeat: matches 3424. .4101 of consensus"

/note="LiPB1 repeat: matches 3424. .4101 of consensus"

/note="LiPB1 repeat: matches 3424. .4101 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consensus,
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//note="L2 repeat: matches 1038. .1144 of consensus"

16851. .17272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1292. 4540
/note="L2 repeat: matches 2321. 2614 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3623. 3937
/note="Alusx repeat: matches 1. 312 of consensus"
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/note="U2 repeat: matches 2. .36 of consensus"
1059. .1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Alusg repeat: matches 54. 310 of cun
12025. 14589
/note="LipBal repeat: matches 243. 3424 of
14524. 14735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1059. 1224
/note="MIR repeat: matches 33. 195 of 2936. 3182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ057385"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="RP11-73304"
/clone_lib="RPCI-11.3"
289. .323
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note="match: GSS:
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Biren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Boguslavkiy, L., Boukhgaller, B. Brown, A.,
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Homo sapiens chromosome 18 clone RP11-403A5 map 18, *** SEQUENCING
IN PROGRESS ***, 3 unordered pleces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159135)
Birren, E., Linton, L., Nusbaum, C. and Lander, F.
Homo sapiens chromosome 18, clone RP11·403A5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(58310, .58614)
/note="match: GSS: Em:B83216"
58331, .58743
/note="match: GSS: Em:AQ890399"
/note="L2 repeat: matches 1543, .1831 of consensus"
/note="L144 repeat: matches 472. .862 of consensus"
//ore="L144 repeat: matches 472. .862 of consensus"
//ore="L144 repeat: matches 472. .862 of consensus"
//ore="L144 repeat: matches 472. .862 of consensus"
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/note="LTR40a repeat: matches 2. .519 of consensus" 47015. .47093 /note="MER91A repeat: matches 105. .186 of consensus" 47500. .47917
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                                                                                                                                            /note="L2 repeat: matches 2309. .2746 of consensus"
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Matches 66; Conservative
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Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Codge, S., Farois, Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illiev, T., Johnson, R., Jones, C., Karatas, A., Lakocque, K., Lu, G., MacLean, C., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McKernan, P., McKernan, K., McPheters, R., Mathews, C., McCarthy, M., Mibova, T., Mlenga, V., Muphy, T., Naylor, J., Nguyen, C., Norbu, C., Morman, C. H., O'Connor, T., O'Oonnell, P., O'Neil, D., Oliver, J., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Retta, R., Kaback, M., Riley, R., Schauer, S., Schupback, R., Sencer, S., Schupback, R., Stencer, S., Schupback, R., Stencer, S., Schupback, R., Stencer, B., Stange-Thomann, N., Travers, M., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, M., Warn, D., Calinoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

AL Submitted (24-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 11, 2001 this sequence version replaced gi:14336523.

All repeats were identified using RepeatMasker:
Smit, A. F.A. & Green, P. (1996-1997)
LILLED C. Connome Conter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 159135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                others
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a 28773 c 28100 g 52128 t 260
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/db_xref="taxon:9606"
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Center clone name: 403_A_5
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Matches 49; Conservative
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Search completed: February 20, 2002, 14:24:46 Job time: 14325 sec

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283.378 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      930621 seqs, 428662619 residues
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	G. Oxydans D-sorbi	buAT. Bos taurus.	Nucleotide sequenc	Human cDNA sequenc	Poly(A) binding pr	Rubella virus RA27	Nucleotide sequenc	Nucleotide sequenc	Human cDNA clone (Human cDNA sequenc	B virus gB glycopr
SUMMARIES			ID	AAX57912	AAQ26664	AAF54723	AAH18235	AAX60227	AAV34766	AAH74659	AAH74658	AAH08593	AAH18316	AAT16474
			DB	20	13	22	22	20	19	22	22	22	22	17
			Length	5187	2640	35465	6045	6002	9759	495	498	781	2540	3177
	o p o	Query	Match Length DB 1	26.8	26.4	25.8	25.6	25.1	25.1	25.0	25.0	25.0	25.0	25.0
			Score	32.4	32	31.2	31	30.4	30.4	30.2	30.2	30.2	30.2	30.2
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	3.5	30.	00		3177	19	AAV331 AAA146	3167 4621	ian herpesvi leotide sequ
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	8 6	30.	9.0	5.5	7607 7623		AAA590 AAT605	76 56	Nucleotide sequenc Plasmid pAdneo-int
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.,,,	62	30.	0,0	N 10	10398		AAT152 AAV221		
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. • • • •	37	30.	7	5	14455		AAV323	7.4	Complete sequence
	88	30.	9.0	N. N	31183		AAA590 AAD039	50 63	Nucleotide sequenc Adenovirus Ad-5 de
. 🤜	0.0	30.	2		31446		AAA090	888	
, ,	117	30.	9.0	N	32026		AAT605 AAA090	59 92	Recombinant adenov AdMMTV-beta-galact
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7 7	5 4	30.	7.0	. v	32166		AAC891	70	on C
							ALIG	ALIGNMENTS	
RESUI AAX50 TD	T 1 7912/c AAX579	1 'c 7912		standard;	d; DNA;	518	7 BP.		
ΧX	~	57912							
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DŢ		JUL-1	6661	(fi	rst entry	rry)			
OE:		oxydan	S	D-sorbi	tol	lehydı	dehydrogenase	coding sequence.	
K K K	D-so L-as	sorbitol		dehydroge acid proc	drogenase producti	on;	sorbose;	2-keto-L-gulonic	acid; precursor;
x so	Gluc	Gluconobacter	acte		oxydans.				
XX	9	92026	63-A	_					
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PF		-0CT-1	-1998	<u>.</u>	8WO-JP0461	04612			
X A H		-0CT-1	-1997;	6	7JP-028	-0285280			
X A	(FUJI	Ē	FUJ	FUJISAWA	PHARM	CO LTD	Θ.		
XX I d	Ishi	i Y,	ž	Noguchi	Υ,	Saito	Y, Soed	da S, Yoshikawa K;	
AA DR	WPI;	199	9.	302741/2	/25.				
AA PT GE PT la		ne group rge-scale ecursor 1	oup a	for Deformed for L-8	r D-sorbitol roduction of L-ascorbic a	of Lo	dehydrogena L-sorbose o	se, useful for r 2-keto-L-gulo	simple nic acid as
X X PS	a	im 21	۵.	age 60	-62; 8	33pp;	Japanes	•	
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Sequence 2640 BP; 456 A; 875 C; 786 G; 523 T; 0 other;

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This sequence encodes the D-sorbitol dehydrogenase of the invention. Cells transformed with a vector containing DNA encoding the dehydrogenase can be used to produce L-sorbose or 2-keto-f.gulonic acid as precursor for simple large-scale L-ascorbic acid production.
                                                                                                                                                                                                2972 GCAGCTGGCAGAAAGAGGCGGCGTATTCCGGCTTTATTCCCCTCACGCATGAAGAAGCTTCTC 2913
                                                                                                                                                                                5 geggeatglacaaagagacegtetacteegeetteaatetgeteatgeatlaceeaeeee 64
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding bovine dopamine transporter protein - useful for diagnosis of Parkinson's disease and related neurological disorders
                                                                                                                                                    0;
                                                                                                                      Length 5187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine dopamine transporter protein; substantia nigra; ss.
                                                                            Sequence 5187 BP; 1251 A; 1390 C; 1297 G; 1249 T; 0 other;
                                                                                                                                                    Indels
                                                                                                                      Score 32.4; DB 20;
Pred. No. 2.1;
0; Mismatches 36;
                                                                                                                                                                                                                                                                         2912 CTTTTCAGGGATGCTGCAACGCGAAGCGC 2883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
361..2439
**tag= a
2606..2612
/*tag= b
                                                                                                                                                                                                                                                 cetegggagcaggcagcaccccagccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 26; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                  AAQ26664 standard; DNA; 2640
                                                                                                                         26.8%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-0782054.
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                        54; Conservative
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                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                AAQ26664;
                                                                                                                            Query Match
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                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                      RESULT
AAQ26664
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The present sequence represents a human polynucleotide sequence, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polynucleotide sequence belonging to the perlecan, precursor of the retinol-binding plasma protein, precursor of the ganglioside GM2 activator, calquanulin B or saposin B protein families. The method is used for detecting, precursor of the ganglioside GM2 activator, calquanulin B or preventing or treating a dependenting or neurological and/or auto-immune disease. The polynucleotides and polypeptides are used for diagnosis, prevention and treatment of multiple scierosis (in its disease, the polynucleotides and polypeptides are used for diagnosis, carious forms and phases). They may also be useful in cases of captured polyarthritis and lupus erythematosus, including use as vaccines and in gene therapy (expression of sense or antisense sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit
                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                        Human, perlecan, retinol-binding plasma protein; calgranulin B; vaccine; ganglioside GMZ activator; saposin B; degenerative disease; glial cell; neurological disease; auto-immune disease; multiple sclerosis; toxicity; Alzheimer's disease; Parkinson's disease; myotrophic lateral sclerosis; rheumatoid polyarthritis; lupus erythematosus; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      retinol-binding plasma protein; calgranulin B; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand
                                                                                       42 tetgetcatgeattacceaecececteqggageagggeageaececeageegeageece 101
                                     Gaps
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Length 2640;
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                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of a human polynucleotide sequence.
   13;
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     DΒ
                                         0; Mismatches
 Score 32;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charles M,
                                                                                                                                                                                                                                                                             AAF54723 standard; DNA; 35465 BP
                                                                                                                                                  102 gctggtaagtggacccgcc 121
                                                                                                                                                                                   942
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     26.4%;
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                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                       923 actgeteggaegeeggee
     Query Match 26.4
Best Local Similarity 62.5
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-159475/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                  AAF54723;
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                                                                                                                                                                                                                                              RESULT
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The present invention describes primer sets for synthesising 5602
[11] length cONAs defined in the specification. Where a primer set
[12] comprises: (a) an oligo-dT primer and an oligonucleotide complementary
[13] comprises an oligo-dT primer and an oligonucleotide complementary
[14] complementary strand of a polynucleotide which complementary
[15] coligonucleotide comprises at least 15 nucleotides; or (b) a combination
[16] of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination
[17] or an oligonucleotide comprises a 5'-end
[18] complementary strand of a polynucleotide which comprises a 5'-end
[18] sequence and an oligonucleotide or printies a 5'-end
[18] sequence and an oligonucleotide comprises at 1 least 15 nucleotides and the complementary
[18] comprises at least 15 nucleotides and the complementary
[18] complementary areas at least 15 nucleotides and the complementary
[18] complementary area useful for synthesisising polynucleotides,
[18] complementary fine primers are useful for synthesisising polynucleotides,
[18] caper threapy. The primers are useful for the
[18] caper threapy. The primers are useful for the proteins encoded by
[18] checkling and/or diagnosis of the abnormality of the proteins encoded by
[18] checkling and or any specialised methods. AAH03166 to AAH1878 and
[18] AAH18633 to AAH18742 represent human cDNA sequences; AAH246 to
                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                       25189 ccaarggccrgrggcarcagaacgaagcacccacrgarrrccgccrgrgcagacccag 25130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                              Gaps
                                                                                    2 ccagoggcatgtacaaagagaccgtctactccgccttcaatctgctcatgcattacccac 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto J;
Length 35465;
                                          ;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito K, Ya
, Otsuki T;
                                                                                                                                                                                              Db 25129 GCCCATAGGGAGCAGGCACGCAGGCTCCTCCGTGGGCACC 25090
  Score 31.2; DB 22;
Pred. No. 6.6;
0; Mismatches 43;
                                                                                                                                                                   62 cccctcgggagcagggagcagcaccccagccgcagcccc 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID 18174; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA sequence SEQ ID NO:18174.
                                                                                                                                                                                                                                                                                                                 AAH18235 standard; cDNA; 6045
    25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                              Conservative
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                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1074617-A2
    Query Match
Best Local Simi
Matches 57;
                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota T, II
Ishii S,
                                                                                                                                                                                                                                                                                                                                                        AAH18235;
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gene which contains a transcribed polymorphic GGG repeat. Albellocation and transcribed polymorphic GGG repeat. Albellocation of the GGC repeat are associated with diseases related with protein (especially polyalanine) accumulation in the mucleus. This is the first description of short trinucleotide repeat expansions causing a human disease. The specification also describes a method for the cuitage of adjacence associated with protein accumulation in the nucleus, comprising obtaining a mucleicacid sample from the patient and determining allelic variants of the GG repeat of the RAB II gene, wherein long allelic variants (245 to 263 bp in longth) are indicative of a disease related with protein accumulation in the nucleus, Allelic variants of the GG repeat of the human RAB II gene are associated with a disease related with swallowing difficulties and protein (preferably polyalanine) accumulation in the nucleus, especially coulopharymgeal muscular dystrophy. The methods can be used to diagnose such diseases, and to develop therapeutics. The present sequence
                                                                                                                                                                 .;
0
AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                         The specification describes a human poly(A) binding protein (PAB) II
                                                                                                                                                                   Gaps
                                                                                                                                                                                                  Human PAB II gene; polymorphic repeat; allelic variant; protein accumulation; polyalanine accumulation; nucleus; trinucleotide repeat expansion; swallowing; coulopharyngeal muscular dystrophy; poly(A) binding protein; ss.
                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allelic variants of the human PAB II gene are associated with
                                                                                                                         Score 31; DB 22; Length 6045;
Pred. No. 5.5;
0; Mismatches 40; Indels
                                                                         Sequence 6045 BP; 1561 A; 1493 C; 1427 G; 1564 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poly(A) binding protein (PAB II) gene sequence.
                                                                                                                                                                                                                                                                                              ccagagactcctgcagccacagctgcagccgcag 786
                                                                                                                                                                                                                                                                             egggageagggaacceecageegeageeceeg 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oculopharyngeal muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 4; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            AAX60227 standard; DNA; 6002
                                                                                                                                Query Match 25.6%;
Best Local Similarity 57.9%;
Matches 55; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-CA01133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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P-PSDB; AAG63606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
AAH74659
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The nucleic acid can be used to identify further attenuated strains of rubbla virus, by sequencing putative strains and determining whether specific attenuating mutation sites are present by comparison with the sequence of RA27/3. Such strains, and the nucleic acid sequence, are useful in vaccines against rubella virus, an important human pathogen. Whilst acute infection is usually benign, infection during early prepancy can result in viral passage across the placenta and replication in the foetus, causing severe birth defects (congenital rubella syndrome, CRS). Eight live attenuated rubella virus vaccines to prevent CRS have previously been developed by serial passage through culture, and vaccine comprising the RA27/3 strain is the most
                                                                                                               62 eccettegggageageageacececageggeagecgeagetggtaagtggaeeeege 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
//raduct= NSP-ORF, nonstructural proteins
//product= NSP-ORF, nonstructural proteins C.E2,E1
//rag= Ap-ORF, virion structural proteins C.E2,E1
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequence for RA27/3 strain of rubella virus - useful to identify further attenuated strains of rubella virus, e.g. for use in vaccines for congenital rubella syndrome
                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                        genomic sequence; viral genome; rubella; RA27/3; vaccine; CRS; congenital rubella syndrome; vaccination; ss.
                                                       Length 6002;
               Sequence 6002 BP; 1405 A; 1340 C; 1697 G; 1559 T; 1 other;
                                                                                     Indels
                                                          20;
                                                                                     56;
                                                          DB
                                                         Score 30.4; DE
Pred. No. 8.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Rubella virus RA27/3 genomic sequence.
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41..6388
/*tag= a
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                                                                                                                                                                                                                                                                          AAV34766 standard; RNA; 9759
                                                         ch 25.1%;
1 Similarity 53.3%;
64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US20399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0030734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW59276, AAW59277.
                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI: 1998-297616/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rubella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9820901-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-1997;
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                                                                                                                                                                                                                                                                                                       AAV34766;
                                                             Query Match
                                                                           Best Local
Matches 6
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                                                                                                                                                                                                                                                               AAV34766
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The present sequence encodes a chimeric fusion protein of the invention. The specification describes a chimeric pIX protein having at least one adenoviral pIX domain and a non-native amino acid sequence. The
commonly used. Genetic characterisation of RA27/3 is also important to assure that the sequence (and therefore the attenuated phenotype) is maintained during vaccine production, and to determine whether complications sometimes occurring after vaccination (e.g. chronic arthritis) are of wild-type or vaccine origin. The nucleic acid may also be used to identify specific attenuating mutation sites, by introducing RA27/3-specific ancleotides into a wild-type infectious clone (e.g. an existing infectious clone based on the Therien strain) and determining whether the resulting virus is attenuated. It may also be used to express RA27/3 in recombinant host cells, by transfecting host cells with the expression vector containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5986 glggacccccgccgagglgggcttgltcggcttccacatcccggtgaagcatgtgagcac 6045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 gtctactccgccttcaatctgctcatgcattacccaccccctcgggagcaggagcagcac 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric plX protein useful in an adenovirus gene transfer vector finfecting cells comprises at least one adenoviral plX domain and a non-native amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  the nucleic acid and culturing the cells under suitable conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of C-terminal fusion protein of pIX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9759 BP; 1458 A; 3775 C; 3008 G; 1518 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pIX protein; chimeric protein; gene transfer vector; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.1%; Score 30.4; DB 19;
57.3%; Pred. No. 9;
iive 0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6046 ccctaccccagcttctgcgggcacgtcggcaccgc 6081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ccccagccgcagccccgctyytaagtggaccccgc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 57.3
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .498
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Gaps

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Indels

38;

Mismatches

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30 etccgcettcaatctgetcatgeattacccaccecectcgggagcagggagcagececea 89
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Conservative
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 53;
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Ishii S,
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  Matches
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non-native sequence is a ligand that binds to a substrate present on surface cells. The chimeric proteins are used for producing adenovirus gene transfer vectors.
                                                                                                                                                                           217 egegggattgtgactgactttgctttcctgagcccgcttgcaagcagtgcagcttcccgt 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric pIX protein useful in an adenovirus gene transfer vector for infecting cells comprises at least one adenoviral pIX domain and a
                                                                                                                          Gaps
                                                                                                                                                    30 etcogoetteaatetgeteatgeattacceaececeetegggageagggeageaecece 89
                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of N-terminal fusion protein of plX protein.
                                                                                                                        0
                                                                                          Score 30.2; DB 22; Length 495;
Pred. No. 6.1;
); Mismatches 38; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                             pIX protein; chimeric protein; gene transfer vector; ss.
                                                       Sequence 495 BP; 84 A; 157 C; 131 G; 123 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "chimeric protein"
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1..498
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                                                                                              Query Match 25.0%;
Best Local Similarity 58.2%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                     AAH74658 standard; DNA; 498
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non-native amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAG63605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oliyo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides or (b) a combination of an oligonucleotide comprises a least 15 nucleotides or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence. Where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the particularly without any specialised methods. Ani03166 to AANI3628 and AANI3633 represent human amino acid sequences; and AANI3629 to AANI3632 of the present plumpur anino acid sequences; and AANI3629 to AANI3632 of the present plumpur anion acid sequences; and AANI3629 to AANI363200 of the present plumpur anion acid sequences; and AANI3629 to AANI36320 of the present plumpur anion acid sequences; and AANI3629 to AANI36320 of the present plumpur anion acid sequences; and AANI36320 to AANI36320 of the present plumpur anion acid sequences; and AANI36320 to AANI36320 of the present plumpur anion acid sequences and acceptance to the present plumpur anion acid sequences and acceptance to the present plumpur acceptance 
                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto J;
T;
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Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 5428; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               likawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                       Human cDNA clone (5'-primer) SEQ ID NO:5428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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Sugiyama T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000EP-0116126
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                           EP1074617-A2
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Length 498;

DB 22;

Score 30.2; Di Pred. No. 6.1;

25.0%; 58.2%;

Query Match Best Local Similarity

0;

Gaps

0;

XX SO

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represent oligonucleotides, all of which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                    61 coccetegggageaggageageaceceageegeageecegetggtaagtggaeeeeg 119
                                                                                                                                                                                                                                                                                                                                          B virus gB glycoprotein and ICP 18.5 kDa protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         simian monkey B virus qB glycoprotein; UL27; diagnosis;
B virus; ICP 18.5 kDa protein; UL28; ss.
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                                                                                                                                                                                   Length 2540;
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                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= ICP_18.5_kDa_protein_fragment
269..2944
/*tag= b
                                                                                           Sequence 2540 BP; 790 A; 519 C; 637 G; 594 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Black D, Eberle R, Hilliard J, Scinicariello F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                              18;
                                                                                                                                                                                      DB 22;
                                                                                                                                                                                      Score 30.2; DB pred, No. 8.1; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= gB_glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SWBI-) SOUTHWEST FOUND BIOMEDICAL RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 3177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes simian monkey B virus.
                                                                                                                                                                                         25.0%;
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                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT16474 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993;
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                                                                                                                                                                                                  0;
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                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                        Yamamoto J;
                                                                                                                                                                                                      ;
                                                                                                                                             Length 781;
                                                                                                                                                                                                         Indels
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Otsuki
                                                           Sequence 781 BP; 231 A; 157 C; 236 G; 154 T; 3 other;
                                                                                                                                                22;
                                                                                                                                                                                                  18;
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A, Naqai K,
                                                                                                                                                DB
                                                                                                                                          Score 30.2; DB
Pred. No. 6.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA sequence SEQ ID NO:18318.
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Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH18316 standard; cDNA; 2540 BP
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T, Wakama
                                                                                                                                             25.0%;
69.5%;
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                Local Similarity 69.5
nes 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length cDNAs
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Ishii S,
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Best Local S
Matches 41
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sample DNA

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Mastadenovirus.
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Prevec L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                          6 eggeatgtacaaagagacegtetaeteegeetteaatetgeteatgeattaceeaeeee 65
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "encodes a fragment of an ICP Protein (UL28)"
                                                                                                                                                   210 caggetegeggeegggggeeegaecageegeecegtageegeegeggegege 264
                                                                                                                                                                                                                                                                                                                                                                                                                             Simian herpesvirus B DNA sequence coding for a gB glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simian herpesvirus B gB glycoprotein; UL27; ICP protein; UL28; differential diagnostic test; immunoassay; antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - coding for gB glycoproteins and
                           Indels
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/product= "gB glycoprotein (UL27)"
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                           53;
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      Pred. No. 8.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWBI-) SOUTHWEST FOUND BIOMEDICAL RES
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                                                                                                                                                                                                                                                                                                     AAV33167 standard; DNA; 3177 BP
      53.9%;
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95US-0541878.
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                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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      Best Local Similarity 53.9
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simian herpesvirus B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-1995;
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10-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-1998
                                                                                                                                                                                                                                                                                                                                             AAV33167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Black D,
                                                                                                                                                        99
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Gaps

0;

Indels

Length 3177;

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The specification describes a recombinant adenovirus that raises an dimmune response against rabies. The adenovirus has a functionally disrupted El region and includes an expression cassette containing DNA that encodes rables glycoprotein, linked to control sequences functional in eukaryotic cells. The adenovirus is used in vaccines against rabies, particularly oral vaccines for protecting wild animals that are vectors of the disease. Incorporation of an intron into the adenovirus prevents homologous recombination with El regions endogenous to have cells. The adenovirus. The present sequence represents a recombinant rabies adenovirus construct AdBHGEB3CA13(1)RG.
                                                                                                                                                                                                                                         Adenovirus; immune response; rabies; El region; glycoprotein; vaccine;
150 egtygtgtacgaccgcgacgtettetecatectetactcggteetgcagcacctggcce 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moore M;
                                                                                                                                                                                                               Nucleotide sequence of a recombinant rabies andenovirus construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein, useful for of wild animals -
                            ctcgggagcaggagcaccccagccgcagccccgctygtaagtggaccccgc 120
                                             Graham FL,
                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "DNA encoding rabies glycoprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3250 BP; 810 A; 740 C; 866 G; 834 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sparkuhl Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2662..2800
/*tag= d
/note= "SV40 polyA sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant adenovirus expressing rabies vaccination against rabies, particularly
                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "HCMV promoter"
                                                                                                                                                                                                                                                                                                                            Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 9a-d; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cassidy K, Yarosh O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MICR-) MICROBIX BIOSYSTEMS INC
                                                                                                                              AAA14621 standard; DNA; 3250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98CA-2246626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0070452
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1051..2
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93WO-US11667
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                  (GENZ ) GENZYME CORP
                                                                               WPI; 1994-200277/24.
P-PSDB; AAR79011-12.
                                                                 Armentano D,
                    03-DEC-1992;
01-OCT-1993;
13-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-NOV-1995
      02-DEC-1993;
                                                                                                                                                                                                                                                                                                                                          53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ91273;
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA091273
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/note= "Represents nucleotides 123-4622 of the published
CFTR cDNA sequence"
                                       Gaps
                             30 etecgeetteaatetgeteatgeattacecacececetegggagcagggcageacececa 89
                                                                                                                                                                                                promoter; E3; p19; MHC; class 1; viral latency; pulmonary airway; ds
                                                                                                                                                                       Recombinant adenovirus; Ad2/CFTR-1; adenovirus 2 serotype; Ela; Elb; viral replication; gene expression; gene therapy; cystic fibrosis; cystic fibrosis transmembrane conductance regulator; CFTR:
                                                                                                                                                                                                                                                                                /*tag= b
/function= E1A enhancer and viral packaging domain
380..500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= 1
/product= 1X protein (Hexon-associated protein)
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Length 3250;
                                                                                                                                                                                                                                                      /rpt_type= INVERTED
/note= "Represents the origin of replication"
190..380
               Indels
                                                                                                                                                                                                                                                                                                                            /*tag= d
/note= "Hybrid EIA-CFTR-EIB message"
499..546
/*tag= e
547..595
                                                                                                                                                                                                                                                                                                                                                               /*tag= f
/note= "Synthetic linker sequences"
DB 21;
               38;
                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "ElA promoter region"
Score 30.2; DF
Pred. No. 8.4;
0; Mismatches
                                                          /*tag= k
/note= "IX protein mRNA"
5201..5623
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/note= "ElB 3' intron"
                                                                                                                                                                                                                                     Location/Qualifiers
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/note= "E1B 3' U'FR"
                                                                                                                                                                                                                                                                                                                                                                                                                 / rag= h
/product= CFTR
5093. 5426
                                                                                                                BP.
                                                                                                                                                           Ad2/CFTR-1 nucleotide sequence.
                                                                                                               AAQ68002 standard; DNA; 5635
25.0%;
58.2%;
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                                                                                                                                             (first entry)
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        1 Similarity 58.2 53; Conservative
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                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                            26-OCT-1995
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                                                                                                                             AAQ68002;
  Query Match
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         Best Local
Matches 5
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                                                                                                RESULT 1
AAQ68002
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This sequence represents the national and Elb regions of the viral genome, which are involved in the early stages of viral replacements and enonvirus A Serctype. The Ela and Elb regions of the viral genome, which are involved in the early stages of viral replication and which are involved in the early stages of viral replication replication. The cystic fibrosis transmembrane conductance regulator (CFTR) coding sequence is inserted into the genome in place of the Ela/Elb region and transcription of the CFTR sequence is driven by the endogenous Ela promoter. This is a moderately strong promoter that is functional in a variety of cells. This adenovirus retains the E3 viral coding region. As a consequence that the growth of the adenovirus-CFTR DNA is greater than that of wild type adenovirus. This renders the DNA more difficult to package and means that provide the missing Ela and Elb functions. The E3 region encodes a number of proteins, including pl9 which is believed to interact with and prevent presentation of MHC class I proteins. This property prevents recognition of the including may allow viral latency. This adenovirus may be administered to the pulmonary airways in the gene therapy of cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 etcogeettcaatetgetcatgeatlacecaceneettoggggggggggggggggcacececa 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the nucleotide sequence of the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                               Adeno:virus-based yene therapy vectors – esp. useful for gene therapy of cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5635 BP; 1619 A; 1142 C; 1324 G; 1550 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
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                                                                                                                                                                                                           Smith AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version of the plasmid vector pAdCMV-HS-Vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.0%; Score 30.2; Di
58.2%; Pred. No. 9.3;
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                                                                                                                                                                                                               Gregory RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 67-80; 167pp; English.
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92US-0985478.
93US-0130682.
93US-0136742.
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                                                                                                                                                                                                               Couture LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                    New adenovirus-5 gene expression system - used for highly efficient, recombinant expression of heterologous genes or gene prods. in host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
25.0%; Score 30.2; DB 16; Length 6120;
Best Local Similarity 58.2%; Pred. No. 9.4;
Matches 53; Conservative 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6120 BP; 1328 A; 1533 C; 1721 G; 1538 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 23; 86pp; English.
/*tag= a
/label= Ad 5 ori
                                                                                                                                           (CORR ) CORNELL RES FOUND INC.
                                                                                                                     93US-0166925.
                                                                                           94WO-US14502.
                                                                                                                                                                                                   WPI; 1995-231566/30.
                                                                                                                                                                          Falckpedersen ES;
                                                                                         14-DEC-1994;
                                                                                                                     14-DEC-1993;
                                      W09516772-A.
                                                                  22-JUN-1995.
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Search completed: February 20, 2002, 14:30:58 Job time: 12447 sec

Appl

Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli

Sequence 15,

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Sequence 1, Appliageduence 1, Appliageduence 1, Appliageduence 1, Appliageduence 9, Appliageduence 1, 
                                     Sequence 1, Approved 1, Approved 1, Approved 1, Approved 43, Approved 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: AMADIMONIN, SANDING STATES OF INVENTION: NOVEL ADENOVIRUS VECTORS TITLE OF INVENTION: FOR GENE THERAPY NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbangh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: A30086A - 2415/31081
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-408-2626
TELEFRAX: 212-765-2519
US-08-549-489-3

US-08-735-609-1

US-08-375-609-1

US-08-379-452-43

US-09-315-372-1

US-09-315-372-1

US-09-4409-670-43

US-09-4409-670-43

US-09-409-670-43

US-09-82-256-9

US-08-939-115-9

US-08-999-733-1

US-08-999-733-1

US-08-933-803A-15

US-08-933-803A-15

US-09-11-410-2

US-09-022-669-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOCTWARE: FSSTEM: DOS
SOCTWARE: FSSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,077
FILING DATE: 06-0CT-1995
CLASSIFFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,874
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Scide, Rochelle K
REGISTRATION NUMBER: 32,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08540077; Patent No. 5824544
GENERAL INFORMATION:
APPLICANT: ROMANCAUK, HELEN
APPLICANT: WADSWOKTH, SAMUEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1796 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                               February 20, 2002, 14:32:12; Search time 162.84 Seconds
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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No
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778 CGCGGGATTGTGACTGACTTTGCTTTCCTGAGCCCGCTTGCAAGCAGTGCAGCTTCCCGT 837

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150 CGTGGTGTACGACCGCGACGTCTTCTCCCATCCTCTACTCGGTCCTGCAGCACCGCCCC 209
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                                                                                                                                                                          APPLICANT: Black, Darla
APPLICANT: Black, Darla
APPLICANT: Scinicariello, Franco
APPLICANT: Hillard, Julia K.
TITLE OF INVENTION: Cloning and Amplification of Monkey B
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/042,747A
                                                                                                                                                                                                                                                                                                                                       SEE: Cox & Smith Incorporated
: 112 East Pecan Street, Suite 2000
San Antonio
Texas
90 gccgcagcccccgctggtaagtggaccccgc 120
                        REFERENCE/DOCKET NUMBER: 35186
REFERENCE/DOCKET NUMBER: S-0072.179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 210-554-5500
TELEFAX: 210-226-8395
TELEX: 767600
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: FLORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            RESULT 3
US-08-042-747A-4
Sequence 4, Application US/08042747A
Sequence No. 5487969
Patent No. 5487969
GENERAL INFORMATION:
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NAME: Haymond, W. Bradley
REGISTRATION NUMBER: 3518
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TELEX: 767609
INFORMATION FOR SEQ ID NO:
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Matches 62; Conserv
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US-08-042-747A-4
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tive 0; Mismatches 38; Indels 0
          Length 1796;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/409,874
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Solde, ROChelle (REGISTRATION INMBER: 33,300
REFERENCE/DOCKET NUMBER: 33,300
REFERENCE/DOCKET NUMBER: A30086A - 2415/31081
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2626
TELEFRAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Brunbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
                                            38;
          DB 1;
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APPLICANT: ROMANCZUY, HELEN.
APPLICANT: WADSWORTH, SAMUEL C.
TITLE OF INVENTION: NOVEL ADENOVIRUS VECTORS
TITLE OF INVENTION: FOR GENE THERAPY
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
      / Match 25.0%; Score 30.2; DE Local Similarity 58.2%; Pred. No. 2.6; les 53; Conservative 0; Mismatches
                                                                                                                                                                                90 geogeageceegetggtaagtggaeeeege 120
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SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,077
FILING DATE: 06-OCT-1995
CLASSIFFTAMEN.
                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08540077 Patent No. 5824544 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 58.2
Matches 53; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ORIGINAL SOURCE:

US-08-540-077-4
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US-08-540-077-4
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CITY: Ne
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                                Best Loca
Matches
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NAME: Hanley, Elizabeth A. REGISTRATION NUMBER: 33,505
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Best Local Similarity 58.29
Matches 53; Conservative
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STATE: MASSACHUSETTS
COUNTRY: USA
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02109
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US-09-248-026-3
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Patent No. 6093367
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: A.E.
TITLE OF INVENTION: ADENOVIRUS VECTORS FOR GENE THERAPY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
STATE: NEW YORK
        Sequence 3, Application US/08136742A
Patent No. 5670488
GENERAL INFORMATION:
APPLICANT: A.E. TITLE OF INVENTION:
TITLE OF INVENTION: GENE THERAPY FOR CYSTIC FIBROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,478
FILING DATE: 02-DEC-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Seide, Rochelle K.
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: 32,300
TELEPRANTION HOWBER: A00668 (Genzyme Dkt. IG4-9.11)
TELECOMMUNICATION HFORMATION:
TELEPRANTION: (212) 408-2500
TELEPRANTION: (212) 408-2509
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5635 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 25.0%; Score 30.2; DB 1; Length 5635; Best Local Similarity 58.2%; Pred. No. 3.3; Matches 53; Conservative 0; Mismatches 38; Indels 0
                                                                                                                                                                         ADDRESSEE: BRUMBAUGH, GRAVES, DONOHUE & RAYMOND STREET: 30 ROCKEFELLER PLAZA CITY: NEW YORK STATE: NEW YORK COUNTRY: USA ZIP: 10112
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,742A
FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-136-742A-3
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US-09-248-026-3
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TITLE OF INVENTION: GENE THERAPY FOR CYSTIC FIBROSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                        SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/248,026
FILING DATE: 10 FEB-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/095,194
FILING DATE: 16 JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Seide, Rochelle K.
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: 33,300
REFERENCE/DOCKET NUMBER: 33,300
REFERENCE/DOCKET NUMBER: 33,0668-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 705-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5635 base pairs
TYPE: NUCLERIC CAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11667
TIVE DATE: 02-DEC-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,478
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application PC/FUS9311667
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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2322 CGCGGGATTGTGACTGCATTGCTTTCCTGAGCCCGCTTGCAAGCAGCAGCAGCTTCCCGT 2381
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                                                                                                                                                                                                                                                 Sequence 1. Application US/08461837
Patent No. 5698202
GENERAL INFORMATION:
APPLICANT: Ertl, Hildegund C.J.
APPLICANT: Milson, James M.
TITLE OF INVENTION: A Replication-Defective Adenovirus Human TITLE OF INVENTION: A Pepplication-Carrier NUMBRR OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Howson and Howson STREET: Spring House Corporate Cntr, PO Box 457 CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
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                                                                                                                                  2382 TCATCGCCCGCGATGACAAGTTGACGGCTC 2412
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                                                                                                        90 geogrageceeegetggtaagtggaeeeege 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REPERENCE/DOCKET NUMBER: UPNH1290USA
TELECOMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08973223 Patent No. 6019978
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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EDNESS: double
3Y: not relevant
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1185..2756
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OPERATING SYSTEM:
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-461-837-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                 US-08-461-837-1
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US-08-973-223-1
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                                                                                                                                                                                                                                                                                                 Score 30.2; DB 5; Length 5635;
Pred. No. 3.3;
0; Mismatches 38; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08374483
Patent No. 5880102
CAPERAL INFORMATION:
APPLICANT: GEORGE, SAMUEL E.
APPLICANT: BLAZING, MICHAEL A.
TITLE OF INVENTION: ADENOVIRAL VECTOR SYSTEM
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5477 TCATCGCCGCGATGACAAGTTGACGGCTC 5507
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      NZI-014CP2
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NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-83
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
TELERAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/374,483 FILING DATE: 17-JAN-1995
REFERENCE/DOCKET NUMBER: NZI-(
TELECHONNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR EQU ID NO: 3:
SEQUENCE CHARACTERIZICS:
LENGTH: 5635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLEGUE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
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Best Local Similarity 58.2%;
Matches 53; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 25.0
Best Local Similarity 58.2
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: lin
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US-08-374-483-1
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nucleic acid
EDNESS: double
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, LOCATION: 1185..2756
US-09-347-060-1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson an
                                                                                  STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                         19477
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PCT-US96-09495-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Indels
                       APPLICANT: Ertl, Hildegund C.J.
APPLICANT: Wilson, James M.
TITLE OF INVENTION: A Replication-Defective
TITLE OF INVENTION: Adenovirus Human Type 5
TITLE OF INVENTION: Recombinant as a Vaccine Carrier
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Erti, Hildegund C.J.
APPLICANT: Wilson, James M.
TITLE OF INVENTION: A Replication-Defective
TITLE OF INVENTION: Adenovirus Human Type 5
TITLE OF INVENTION: Recombinant as a Vaccine Carrier
NUMBER OF SEQUENCES: 2
                                                                                                                                                                ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.0%; Score 30.2; DE Best Local Similarity 58.2%; Pred. No. 3.5; Matches 53; Conservative 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,837
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/000,078
FILING DATE: 08-JUN-1995
ATTORNEY/AGENT INFORMATION:
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Patent No. 6287571
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BAK, MATY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UPNE
TELECOMMUNICATION INFORMATION:
TELEPRIONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ 1D NO: 1:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 8236 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1185..2756
                                                                                                                                                                                                                                   Pennsylvania
          GENERAL INFORMATION:
                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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US-08-973-223-1
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US-09-347-060-1
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APPLICANT: Ertl, Hildegund C.J.
APPLICANT: Wilson, James M.
TITLE OF INVENTION: A Replication-Defective Adenovirus
TITLE OF INVENTION: Human
TITLE OF INVENTION: Type 5 Recombinant as a Vaccine Carrier
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
SEE: Howson and Howson
: Spring House Corporate Cntr, PO Box 457
Spring House
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Howson and Howson
Spring House Corporate Cntr, PO Box 457
                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/347,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.0%; Score 30.2; D 58.2%; Pred. No. 3.5; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/461,837 FILING DATE: 05-JUN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/000,078 PILING DATE: 08-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS9609495
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/973,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UF
TELECOMONIOTATION INFORMATION
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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STREET: St
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Karen F.
APPLICANT: Strauss, Jerome F.
TITLE OF INVENTION: Methods and Compositions for Gene
TITLE OF INVENTION: Therapy for the Treatment of Defects in Lipoprotein
TITLE OF INVENTION: Metabolism
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4913 CGCGGGGTTGTGACTTTGCTTTCCTGAGCCCGCTTGCAAGCAGCAGCAGCAGCTGCGGT 4972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.0%; Score 30.2; DB 1; Length 9592; 58.2%; Pred. No. 3.6; tive 0; Mismatches 38; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spring House Corporate Cntr., PO Box 457
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                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,734
FILING DATE: 24 FEBT 1995
ATTORNEY AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.009CIPIUSA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4973 TCATCCGCCGCGATGACAAGTTGACGCTC 5003
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                                                                                       APPLICATION NUMBER: US/08/393,734
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                                                                                                                                                                          NAME: BAK, MATY E.
REGISTRATION NUMBER: 31,215
REFRENCE/DOCKET NUMBER: UPNHIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEPHONE: 215-540-9208
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 9592 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 25.09
Best Local Similarity 58.29
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Spires
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown MOLECULE TYPE: CDNA US-08-393-734-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                                                    FILING DATE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wilson, Jerome F.
APPLICANT: Strauss, Jerome F.
APPLICANT: Strauss, Jerome F.
APPLICANT: TITLE OF INVENTION: Methods and Compositions for Gene
TITLE OF INVENTION: Methods in Lipoprotein
TITLE OF INVENTION: Metabolism
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3557 CGCGGGATTGTTGTTTTGCTTTCCTGAGCCCGCTTGCAACCAGTGCAGCTTCCCGT 3616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 3.5;
0; Mismatches 38; Indels 0
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                                                                                                                                           COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 3617 TCATCCGCCGCGATGACAAGTTGACGCTC 3647
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UPNH1290APCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 geogeageeecegetggtaagtggaeeeege 120
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APPLICATION NUMBER: US 08/461,837
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,078
FILING DATE: 08-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/08393734
; Patent No. 5652224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 58.2%;
Matches 53; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
1185..2756
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                  Spring House
Pennsylvania
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                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
PCT-US96-09495-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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5719 CGCGGGATTGTGACTGTTGCTTTCCTGAGCCCGCTTGCAGCAGTGCAGCTTCCCGT 5778
30 etccgcettcaatctgctcatgcattacccaccccctcgqqagcagggggggacccca 89
                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08331384
Sequence 1, Application US/08331384
Sequence 1, Application US/08331384
Sequence 1, S856152
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Kelley, William M.
APPLICANT: Fisher, Krishna J.
TITLE OF INVENTION: Hybrid Adenovirus-AAV Vector and Methods TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/331,384 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,215
REFERENCE/CDCKEF NUMBER: UPN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-5818
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.0%;
Best Local Similarity 58.2%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 10398 base pairs
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STATE: Pe
COUNTRY:
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CURRENT APPLICATION DATA:
PELLIAN DATA:
PELLIAN DATE:
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PAME:
PERTICATION NUMBER:
PERTICATION NUMBER:
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PELECOMMUNICATION INFORMATION:
TELECHONE:
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                                                                                                                                                                                                                                                                                                                                                                        25.0%; Score 30.2; DB 4; 58.2%; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GEORGE, SAMUEL E.
APPLICANT: BLAZING, MICHAEL A.
IITLE OF INVENTION: ADENOVIRAL VECTOR SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%; Score 30.2; DE
ilarity 58.2%; Pred. No. 3.6;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08374483
Patent No. 5880102
                                                 INFORMATION FOR SEC 10 NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 9592 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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LENGTH: 9641 base pairs
                           215-540-9200
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Matches 53; Conservative
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STRANDEDNESS: single
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: AD NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            TOPOLOGY: unknown;
MOLECULE TYPE: CDNA
US-08-894-489-3
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BG38G035 602455204
BG655501 184802.x
B1154476 602904810
BB584341 BB584341
BF79331 RC6-C1012
A1049127 ub35d04.r
A113784 uc37a06.r
A0137897 HZ.3058_B
BF53482 6020539B
BF53482 6020539B
BF534635 PM1-EN006
                                                                                February 20, 2002, 13:52:27 ; Search time 3793.25 Seconds
(without alignments)
342.777 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                          11351937 seqs, 5372889281 residues
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Maximum Match 100%
Listing first 45 summaries
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BG386035
BG685601
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AF799331
AA958693
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                                                         OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                    Run on:
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AV070409	BG793616	BB608462	AZ049530	AI657239	BF696719	A0744189	BE871820	BF578750	AA055704	F11815	AA511221	BE785913	BG326641	B47161	BF063108	AQ332734	AZ593838	B1227246	BF621610	BF864875	AQ483120	BE512646	BE787988	BF342437	CNS010AP	BE163170	929	39	W97467	535	AA049789	W12086	
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192	589	266	474	555	842	952	1069	728	218	285	436	692	1002	262	458	473	607	648	861	1293	699	1068	1110	1187	1201	244	274	309	354	374	377	403	
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ALIGNMENTS

A311787	
OCUS	AA311787 273 bp mRNA EST 19-APR-1997
DEFINITION	EST182503 Jurkat T-cells VI Homo sapiens CDNA 5' end similar to
	similar to T-cell factor 1, A/B/C, mRNA sequence.
ACCESSION	AA311787
FERSION	AA311787.1 GI:1964114
KEYWORDS	EST.
SOURCE	liuman .
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 273)
AUTHORS	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
	, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
	,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
	Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
	,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
	<pre>Gnebm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,</pre>
	Kelley,J.C., Liu,L1., Marmaros,S.M., Merrick,J.M.,
	Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
	Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
	Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
	Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
	Dimke, D., Feng, DF., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.
	, Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
	Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
	Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
	, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
	Venter, J.C.
TITLE	Initial assessment of human gene diversity and expression patterns
	based upon 83 million nurleotides of cDNA sequence
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)
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/lab_host="DH10B (phage=resistant)"
/note="Organ: colon; Vector: pOTB); Site_1: Xho1; Site_2:
ECORI: cDNA made by oligo-dT priming. Directionally
                                                                                              Email: arkeriavetigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi/hdi)
Seq primer: M13 Reverse.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Calarrhini; Hominidae; Homo.
1 (bases 1 to 353)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact Robert Strausberg, Ph.D.
Email: cgapbs r@mall.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                       BG386035 353 bp mRNA EST 12-MAR-2001 602455204F1 NIH_MGC_15 Homo sapiens CDNA clone 1MAGE:4583473 5'
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             The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Pred. No. 1.8e-15;
0; Mismatches 2;
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    .273
    /organism="Homo sapiens"

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/db_xref="taxon:9606"
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High quality sequence stop: 276.
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/clone_lib="NIH_MGC_15"
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Best Local Similarity 98.1%;
Matches 103; Conservative
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Bloinformatics
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TITLE
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BG386035
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG655601 400 bp mRNA EST 05-JUL-2001 is 48402.xl Melton Mouse E16 5 Pancreas Library M1621 Mus musculus cDNA 3' similar to SW.TCF1 MOUSE 000417 T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: dmeiton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone pleases contact: Juliana Brown
(brown@fas.harvard.edu)
cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)" at 11 c 12 g 40 t.
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/clone_lib="melton Mouse E16 5 Pancreas Library M1621"
/sex="Both"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 ACCAGCGCATGTACAAAAAGACGTCCTCTACTCCGCCTTCAATCTGCTCATGCATAACCA 252
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Seq primer: -40UP from Gibco
High quality sequence stop: 394.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 88.4; DB 11;
Pred. No. 5.9e-12;
0; Mismatches 1;
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/dev_stage="Embryonic day 16.5"
/lab_host="TOP10"
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/strain="ICR"
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oligo-dT priming. XhoI site destroyed during cloning. Size-selected by column fractionation; average insert size 1.2kb. Primary library, unamplified."
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602904810F1 NIH_CGAP_Mam3 Mus musculus CDNA clone IMAGE:5034194 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 649)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Lothar Henrighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                    62 ececetegggagcaggcagcaccecagecgcageccecgetggtaagtggaccecgee 121
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Pred. No. 2.6e-11;
0; Mismatches 22; Indels 0
                                                                                                                                                 Length 400;
                                                                                                                                                                                       20; Indels
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/lab_host="DH10B"
                                                                                                                                               Score 88; DB 11;
Pred. No. 7.5e-12;
0; Mismatches 20;
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Plate: LLAM11095 row: d column: 03
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Location/Qualifiers
1. .649
/organism="Mus musculus"
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/clone="IMAGE:5034194"
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ilarity 81.8%;
Conservative 0
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Best Local Similarity 83.3%;
Matches 100; Conservative (
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Bammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Theses 1 to 264)
RS Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Rawai, J., Kojima, Y., Konno, H., Kisakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, C., Sakai, C., Sakai, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Shirata, T., Sagakei, T., Yamaki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Watahiki, A., Wamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.
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URL.http://genome.gsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp/
Carninci,P., Wishiyama,Y., Westover,A., Itoh,M., Naqaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and tisa application for the synthesis of full length
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
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system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (HIKEN)
The Institute of Physical and Chemical Research (HIKEN)
Tel: 81-45-503-922
Fax: 81-45-503-9216
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Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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BB584341 264 bp mRNA EST 30-NOV-2000 BB584341 RIKEN full-length enriched, adult male epididymis Museulus cDNA clone 9230105F22 5', mRNA sequence.
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/dev_stage="adult"
/lab_host="DH10B"

    .264
    /organism*"Mus musculus"

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/clone="9230105F22"
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Contact: Yoshihide Hayashizaki
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIO49127 288 bp mRNA EST 08-JUL-1998 ub35d04.rl Scares thymus_ZNDMT Mus musculus cDNA clone IMAGE:1379719 5' similar to gb:X59869 TRANSCRIPTION FACTOR-7 (HUMAN); gb:X61385 Mouse mRNA for T-cell specific transcription factor
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                      /dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: colon_ins; Vector: puc18: Site_1: Smal;
//note="Organ: colon_ins; Vector: puc18: Site_1: Smal;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 288)
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                     Length 201;
                                                                                                                                                                                                                                                                                                                                                                  54.5%; Score 66; DB 11; Length 20: 100.0%; Pred. No. 1.4e-06; ive 0; Mismatches 0; Indels
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Contact: Marra MyMouse EST Project
Washb-HHM Mouse EST Project
Washington University School of MedicineP
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/sex="male"
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/clone="!MAGE:1379719"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone_lib="CI0122"
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Buraryota i Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Buraryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201)

10 Sas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.P., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-CI0122-091000-021-D10&t3=2000-01-09&t4=1)
Seq primer: puc 18 forward
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            Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGAGAGGACCTTTTTTTTTTTTTVN 3'], CDNA was
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RC6-C10122-091000-021-D10 C10122 Homo sapiens CDNA, mRNA sequence.
BF799331
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 3.6e-09;
0; Mismatches 27; Indels 0;
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/db_xref="taxon:9606"
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High quality sequence stop: 201
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ilarity 77.5%;
Conservative (
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Fax: +55-11-2707001
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Query Match
Best Local Similarity
Matches 91; Conserv
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AA958693 330 bp mRNA EST 08-MAY-1998
V34111:11 Soares_thymus_ZNDMT Mus musculus cDNA clone
IMAGE:1344933 5' similar to gbh:X59869 TRANSCRIPTION FACTOR-7 (HUMAN); gb:X61385 Mouse mRNA for T-cell specific transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tobases 1 to 330)
Marra,M., Hillier,L., Allen,M., Howles,M., Dietrich,N., Dubuque,T., Sclesle,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoce,M., Tan,F., Underwood,K., Moore,H., Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Mammalia; Eutheria, Rodentia; Sciurognathi, Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNI, ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:693725
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                                                                                                                                                                                                        Ouery Match 51.9%; Score 62.8; DB 10; Length 288; Best Local Similarity 75.8%; Pred. No. 8.6e-06; Matches 91; Conservative 0; Mismatches 27; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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/b_xref="taxon:10090"
/clone="thAGE:1344933"
/clone="thAGE:1344933"
/clone="thAGE:174933"
/clone="thAGE:174933"
/clone="thAGE:174933"
/clone="thAGE:17493"
/clone="thAGE:17493"
/dev_stage="thAGE"
/lab_lost="bH108"
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High quality sequence stop: 167.
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/organism="Mus musculus"
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                                                                                                                                    108 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOUSE);, mRNA sequence.
AA958693
AA958693.1 GI:3124923
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SOURCE

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/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oliqu(dT) primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marral, Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                           1;
3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertirand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A131784 152 bp mRNA EST 14-SEP-1998 uc37a06.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1400146 5' similar to 9b:X61385 Mouse mRNA for T-cell specific transcription factor (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                             2 ccagcggcatgtacaaaqagaccgtctactccgccttcaatctgctcatgcatlacccac 61
                                                                                                                                                                                                                                                                                                                                 Gaps
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Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                           Length 330;
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/clone_lib="Scares_mammary_gland_NbMMG"
/sex-"male"
                                                                                                                                                                                                                                                                     Score 62.8; DB 10;
Pred. No. 8.7e-06;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                 51.9%;
ilarity 75.8%;
Conservative
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 587).

INIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Louppublished (1999).

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LLNL.)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:4193012"
/clone="lp="NCI CGAP_SG2"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: salivary gland; Vector: pcMV-SPORT6; Site_1:
/notis Site_2: Sali; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 411)
Dias Neto, F., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
                                                                                                                                                                                                       BF538482 587 bp mRNA EST 11-DEC-2000 602053985F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4193012 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF846035 411 bp mkNA EST 16-JAN-2001
PM1-EN0060-151000-001-d11 EN0060 Homo sapiens CDNA, mRNA sequence.
BF846035
258 CCAGGGGAGTGGAGAATTATCCTGTCTCATTGGAGTTCCAGGTGCTGCTGGATTACGAAA 317
                                         62 eccettegggagcaggagcagcaccecagccgcagccgctggtaagtggaccecg 119
                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 27.9%; Score 33.8; DB 11; Length 587; L Similarity 84.4%; Pred. No. 88; 38; Conservative 0; Mismatches 7; Indels 0
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High quality sequence stop: 587.
Location/Qualifiers
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/strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                   BF538482.1 GI:11625850
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BF846035/c
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  T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko. Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Adams, M.D.
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/db.zref="taxon:9606"
/clone="plate=3058 Col=4 Row=p"
/clone=lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                                                                  Length 152;
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ilarity 55.9%; Pred. No. 49;
Conservative 0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 465)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Sequencing Center
High Throughput Sequencing Center
High Throughput Sequencing Center
High Throughput Sequence Name North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Exa: (206) 616-3887
Exa: (206) 616-3887
Exa: (206) 616-3887
Exail: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3058
Fow: P Column: 4
                                                                                                                                                                                                                                                                               23; Indels
                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                Score 52.2; DB 1
Pred. No. 0.0029;
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                                                                                                                                                                                                                                                                               0; Mismatches
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Location/Qualifiers
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                                                                                                                                                                                                                                  ch 43.1%;
1 Similarity 74.2%;
66; Conservative
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s 56 c
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Gaps

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Lupublished (2001)
Contact: Schageman JJ
Schageman JJ
Contact: Schageman JJ
Contact: Labs
Shohet/Garner Labs
University of Texas Southwestern Medical Center
University of Texas Southwestern Medical Center
6000 Harry Hines Blvd., NA2.226, Dallas, TX 75390, USA
Tel: 214 648 1674
Email: Jeff.Schageman@UTSouthwestern.edu
cDNA library constructed by UTSW as a component of the Program for
Genomic Applications (PGA) and the Reynolds Heart Disease
Genomic Applications (PGA) and the Reynolds Heart Disease
prevention grants for use in cDNA microarray experiments. Sequence
Quality: Sequence ends were trimmed based on percentage of ambigu
us base calls or 'N's in windowed seqments. Sequencing: Rirst-pass
sequencing: ABI Prism 377 sequencer and analysis software.
Seq primer: MI3/PuC Reverse.
                                                                                                           Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermostabilization
trehalose and its application for the synthesis of full length cDNA
trehalose and its application for the synthesis of full length cDNA
transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG793616 589 bp mRNA EST 16-MAY-2001
UTSW_SM14B2 UTSW Adult Mouse Skeletal Musche Library Mus musculus
CDNA clone UTSW_SM14B2, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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/clone="2010318F14"
/clone_lib="Mus musculus small intestine C57BL/6J adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 589)
Gallardo, T.D., Schageman, J.J., Pertsemlidis, A., Garner, H.R.,
Williams, R.S. and Shohet, R.V.
UT Southwestern Medical Center, Adult Mouse Skeletal Muscle CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 accagoggcatgtacaaagagacogtotactocgcottcaatotgctcatgcattacoca 60
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                                            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.6; DB 10;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="small intestine"
/dev_stage="adult" 51 9 61 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
Genome Science Laboratory
RIKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                           Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Conservative
                                                                                                                                                                                                                                                                                  further details.
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Best Local Similarity
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/do_xref='taxon:9606"
/do_xref='taxon:9606"
/clone_lib="EN0060"
/dev_gtage="Adult"
/note="Organ: lung_normal; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196, 7716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA, amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sertry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMIst2=PMI-EN0060-
151000-001-dl1st3=2000-10-15st4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV070409 Mus musculus small intestine C57BL/6J adult Mus musculus cDNA clone 2010318F14, mRNA sequence.
AV070409
AV070409.1 GI:5190237
                   Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H. Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                expressed
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                                                                                                              Shotgun sequencing of the human transcriptome with ORF
                                                                                                                sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           low stringency conditions."
86 c 151 g 109 t
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High quality sequence start: 9
High quality sequence stop: 407.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
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Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 71.79
Matches 43; Conservative
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/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was GAGAGAGAGCGCCGCAACTCGAGTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 65~\rm c 105~\rm g 52~\rm t
                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="8330005117"
/clone_lib="RIKEN full-length enriched, 2 days pregnant
adult female ovary"
Carninci,P. and Hayashizaki,Y. High-cefficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 ATAGACACCTTCAACCCGTTCATCCACCCGCTAGTACATTUGGGCGGGCTTUCGCGCGGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 aaagagaccgictaciccgccitcaaictgcicaigcaitacccaccccccicgggagca 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="ovary"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 gggcagcaccccagccgcagcccccgctggtaagtggacccg
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                                                                                                                   Location/Qualifiers
                                                                                               details
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Matches 59; Conserv
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Primer: Oligo dr. RNA Isolation: cytoplasmic RNA preps
Mannialis); Cloning Technique: CUA Cloning (CloneAmp.
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCACTGAATTCTGAGTG-->. Other
information regarding entire library may be found at
http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar
ies.htm."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-reségsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.p., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Hermostabilization and thermoatilvation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayshizaki, Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB608462 266 bp mRNA EST 06-DEC-2000 BB608462 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330005117 5', mRNA sequence. BB608462
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="UTSW_SM14B2"
/clone="In="UTSW Adult Mouse Skeletal Muscle Library"
/sex="Pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                            /tissue_type="Diaphragm/Hind limb muscles"
/cell_type="Skeletal muscle"
/dev_stage="2 months"
/lab_host="DH5a"
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                                                                                                                                                                                                                                                                                                                                                                                                            5 others
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Pred. No. 1.9e+02;
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ORIGIN
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February 20, 2002, 11:02:39 ; Search time 1729.17 Seconds (without alignments) 171.729 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2944280
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1472140 seqs, 8248589755 residues
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                                                                                                                        OM nucleic - nucleic search, using sw model
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                           Run on:
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SUMMARIES

- :	AC060773 Homo sapi	AC005658 C1tD_11_0	AC0081/3 HOMO SEPT AC005659 citb 161_	AL359833 Human DNA	AL356419 Human DNA	AC091699 Homo sapi	G66013 SY890 Misce	247361 H.sapiens T 247362 H.sapiens T	X59869 Human TCF-1	X59870 Human TCF-1	x63901 Homo sapien x59871 Human TCF-1	AI,050312 Human DNA	Al.133231 Human DNA	ACU/4135 HOMO Sapi ACU68850 Homo Sapi	AC010286 Homo sapi	AC036189 Homo sapi	AC011502 Homo sapi	AC002420 Human Chr	AC004814 Homo sap1 AT.035398 Human DNA	AC009012 Homo sapi	AC011336 Homo sapi	ACOUNTY MONO SAPT	AC013652 Homo sapi	AC004929 Homo sapi	AC010880 Homo sapi	AC012611 Homo sapi	ACOII446 HOMO SAPI ACO21083 HOMO SADI	AL157699 Human DNA	AC009829 Homo sapi	ACU63773 HOMO SAPI ACU05809 Homo sapi	AC010072 Homo sapi	ACO68398 Homo sapi	AL161724 Human DNA	47.8		09-MAY-2001	WORK IN		EULLAOP.		raniata; Vertebrata; Euteleostomi; atarrhini; Hominidae; Homo.	and Lander, E.	RP11-741G21	A.	, Bastien,V., Beda,F., rown,A., Burkett,G.,
ID												HSTCF LC HSBA9F1	AL13323	AC07413	AC01028	AC03618	HS179D3	AC00242	AC00481	AC00901	AC01133	AC01617	AC01365	AC00492	ALI5884	AC01261	AC01144	AC02108 AL15769	AC00982	AC08377	AC01007	AC06839	AC008508 AL161724	ALIGNMENT			p DNA some 4 c	ed pi	61518 urgs DRAFT: HT		Chordata; Cra Primates: Ca	S) Nusbaum,	ome 4, cl	115) Nusbaum.C	Win, J., Barna, Joukhgalter, B.,
DB																																	0 0			1	a S	der	20		oa;	20291	ОШО		
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ue:	! -	94.	94.	9,46	94.	94.	9.4	91.		91.	91.	91.	91.	91.			91	91	91	91	91.1	91	2 2	91	<u>6</u> 9	91	9.1	91	91	20.0	91.1	1 91.1	91.1				AC060773 Homo sapi	EQUENCE,	AC060773.3 GI	human.	Homo sapien Eukaryota; Mammalia: F	(bases	Omo sap	2 (bases 1	Anderson, S. Boguslavkiy
Score		1 ~	-	٦,-		Н,	161	16.		16.	16.	16.	16.	16	910	16.	16	16.	16.	9 -	16	16.	16	16.	16.	16.	16.	16	16.	16.	16	16	16.4 16.4			7 0	NO	_	_		Σ				
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Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Poyle, M., Ferreira, P., FitzHugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahum, L., Grand-Pierre, M., Grant, G., Hagos, B., Haeford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Locke, K., Macdonald, P., Marquis, N., McZarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McTatlim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Doniell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Frange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vons, G., Zainoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W. J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W. J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Subramaniasion A. Intert Submission

AL Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 10, 2001 this sequence version replaced gi:7798794.

All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 741_G_21

Center clone name: 741_G_21

Center clone name: 741_G_21

Sequencing vector: M13: M7915; 49% of reads
Sequencing vector: Plasmid: n/a: 51% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.960731

Consensus quality: 201020 bases at least 040

Consensus quality: 201020 bases at least 030

Consensus quality: 201085 bases at least 020

Insert size: 104000; agarose-fp

Insert size: 104000; agarose-fp

Insert size: 10215; sum-of-contigs

Quality coverage: 9.5 in 020 bases; agarose-fp

Quality coverage: 9.1 in 020 b.

NOTE: This is a "working draft' sequence. It currently
consists of 8 contigs: The true order of the pieces

is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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144532 184185: contig of 39654 bp in length
184186 184285: gap of 100 bp
184286 202915: contig of 18630 bp in length.
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Direct Submission
Submitted (10-SEP-1998) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02154, USA
3 (bases 1 to 72449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-OCT-1998) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA 4 (bases 1 to 72449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-NOV-1999) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02164, USA Vector Sequence Clipped on Nov 5, 1999 this sequence version replaced gi:4314336.
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Smith, D.R.
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                                                                                                                                                                                                                                                                                                                                               707 others
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
/clone="RP11-741G21"
/clone_lib="RPCI-11 Human Male BAC"
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37018 c 37733 g 65883 t
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Pred. No. 23;
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5649. 7747
/note-massembly_fragment"
7848. 7566s
/note-massembly_fragment"
75766. 1109526
/note-massembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
184286. .202915
/note="assembly_fragment
                                              /note="assembly_fragment
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing of Human Chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      citb_11_o_6, complete sequence. AC005658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith,D.R.
Direct Submission
Submitted (02-MAR-1999) Genome
Street, Waltham, MA 02154, USA
5 (bases 1 to 72449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                             vector_side:left"
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Smith, D.R.
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                                                                                             5548
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                             4060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Best Local Similarity
Matches 18; Conserv
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COMMENT

/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="4"

source

05-NOV-1999

PRI

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Sequencing of Human Chromosome 10
Unpublished
2 (bases 1 to 116058)
2 (bases 1 to 116058)
Smith, D.R.
Direct Submission
Submitted (10-SEP-1998) Genome Therapeutics Corporation, 100 Beaver Street, Maltham, MA 02154, USA
3 (bases 1 to 116058)
Smith, D.R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 116058)
Smith, D.R.
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34107 a 26479 c 25708 g 29764 t
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/chromosome="10"
                                                                                                                              AC005659 116058 bp DNA
Cibb_161_9_12, complete sequence.
AC005659.3 GI:6249677
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1. .116058
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Street, Waltham, MA 02154, USA
Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing Technology. Data may contain low quality seq uence and BAC/Cosmid vector sequences.

* NOTE: This is a 'working draft' sequence. It currently contaists of 3 contigs. Gaps between the contigs.

* NOTE: This is a 'working draft' sequence. It currently contaists of 3 contigs. Gaps between the contigs.

* NOTE: This believed to be correct as given, however the sizes

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.

* This sequence as soon as it is available and

* the Afolysing of 2074 bp in length

* 4553 73522: contig of 88970 bp in length.

* 173522.

* Location/Qualifiers
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 73522)
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                                                  /organism="Homo sapiens"
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/4 a 15799 c 16718 g 21138 t
                                                                                                                                                                                                                      Query Match 94.4%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 90; Matches 17; Conservative 0; Mismatches
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/organism="Homo sapiens"
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/clone="C1T987SK-1161G12"
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Best Local Similarity 100.0%; Pred. No.
Matches 17; Conservative 0; Mismatch
                Location/Qualifiers
1. .72449
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2 (bases 1 to 73522)
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Beaver

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Length 116058; Indels

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/note="L1MA3 repeat: matches 5890. .5951 of consensus"
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/note="match: GSS: Em:A0712657"
17575. .17763
/note="match: GSS: Em:A0712657"
/note="MaRR3 repeat: matches 2. .189 of consensus"
n 1826. .18366
/note="L2 repeat: matches 2629. .2701 of consensus"
18338. .18454
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/note="MIR repeat: matches 41. .204 of consensus"
18922. .19041
/note="MIR repeat: matches 1. .120 of consensus"
10042. .19353
/note="MIR repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22031. .22133
//note="L2 repeat: matches 2588. .2709 of consensus"
//note="122344
/note="17 copies 2 mer tt 88% conserved"
25897. .25952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matches 2263. .2453 of consensus" 13150. .13312
//note="MMR repeat: matches 26. .206 of consensus" 14843. .15369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L2 repeat: matches 2416. .2502 of consensus"
21398. .21503
                                                                                                                                                                      /note="MLTID repeat: matches 1. .505 of consensus" 10665. .10733 /note="L2 repeat: matches 2673. .2749 of consensus" 10810. .11093
                    .2184 of consensus"
                                                                                                                                                                                                                                                                                                                                          .2678 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluJo repeat: matches 34. .307 of consensus"
12080. .12295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 120, .252 of consensus" 20467, .20574
                                                                                                                                                                                                                                                                                       .284 of consensus"
                                                                                                                        .280 of consensus"
                                                                                                                                                                                                                                                                                                                                                                 11492. .11812
//note="AluY repeat: matches 1. .311 of consensus"
11813. .12079
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21919. .21981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /noce="12 copies 3 mer atg 86% conserved"
17125. 17345
**Conter="Mills repeat: matches 8. 256 of consensus"
complement(17254. 17781)
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26865. 26958
/note="MIR repeat: matches 2. 96 of consensus"
1793. .27478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="27 copies 4 mer aaag 70% conserved"
21001. .21096
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30489: 30554
/note="33 copies 2 mer aa 66% conserved"
31186: 31219
/note="17 copies 2 mer gt 85% conserved"
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27482. .27618
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complement(8619. .9104)
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11492. .11812
                                                                                                    /note="AluSx repeat: matches 1. 9394, .9911
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11275. .11491
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match: GSS: Em:A0347511"
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complement(27740. .
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                                                                                                    Submitted (123-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire, Submitted (123-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 24, 2000 this sequence version replaced gi:11225780.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: numbers given in the feature table with their source databases: on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence thtp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chrl
RP11-18669 is from the library RPCI-11.1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP11-186C9 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-186C9 is at 122014 in this sequence. The true left end of clone RP11-421L10 is at 754 in this sequence. The true right end of clone RP11-431022 is at 120 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2728 of consensus"
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70cl="LilM4 repeat: matches 2956. .3318 of consensus"

7233. .4310

70cle="LilM4 repeat: matches 4840. .4930 of consensus"
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/note="10 copies 4 mer gaaa 80% conserved"
5403. .5682
/note="Alusx repeat: matches 1. .276 of consensus"
6453. .6706
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note="AluSx repeat: matches 1. .312 of consensus"
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complement(6516. .6989)
/note="match: GSS: Em:AQ798812"
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 122014)
Hall,R.
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1644. .2026
/note="LIMEc repeat: matches 1499.
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note="MLTIB repeat: matches 1.
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/note="match: GSS: Em:AQ559088"
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877. 1115
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11.1"
122. .461
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us-09-904-420a-9.rge

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On Jul 19, 2001 this sequence version replaced gi:14268075.

During sequence assembly data is compared from overlapping clones, where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL: Sw: SWISSPROT; Tr: TREMBL: WHEW WORMPEP: Information on the WORMPEP the Common whis common and the worman and attabase can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/HGP/Chr10
RP11-99L6 is from the library RPCI-11.1 constructed by the group of RP11-99L6 is from the library RPCI-11.1 constructed by the group of Perfect a Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
WECTOR: pBACe3.6
RP11-99L6 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RP11-99L6 is at 120232 in this sequence. The true left end of clone RP11-328K15 is at 107108 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
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/note="MIT1H repeat: matches 493. .534 of consensus"
3737. .3932
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// note="L2 repeat: matches 2579. 2690 of consensus" 1608. 1901
// note="AluJo repeat: matches 17. 307 of consensus" 2656. 2726
// note="MIIII repeat: matches 72. 143 of consensus" 2864. 2959
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/note="Alusq repeat: matches 1. .311 of consensus"
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/note="AluSx repeat: matches 1. ,307 of consensus"
/1184. 1306
//note="FLAM_C repeat: matches 4. ,124 of consensus"
1495. 1600
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/note="MLT2B repeat: matches 1. .448 of consensus"
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8878. .9427
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="RP11-991.6"
/clone_11b="RPCI-11.1"
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/note="L2 rep
5527. .5837
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Human DNA sequence from clone RP11-99L6 on chromosome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7010-*AluJb repeat: matches 1. .295 of consensus."
7701-*AluJb repeat: matches 1. .295 of consensus."
7701-*MLTIF repeat: matches 56. .233 of consensus."
7701-*MLTIF repeat: matches 232. .460 of consensus."
7701-*MLTIF repeat: matches 232. .460 of consensus."
7701-*MLTIF repeat: matches 232. .460 of consensus."
7701-*MLTIF repeat: matches 485. .533 of consensus."
7701-*MLTIF repeat: matches 2591. .2750 of consensus."
7701-*MLTIF repeat: matches 2591. .2750 of consensus."
7701-*L2 repeat: matches 2591. .2750 of consensus."
7701-*L2 repeat: matches 2310. .2470 of consensus."
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Direct Submission
Submitted (18-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CEB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1M4 repeat: matches 3812. .4238 of consensus"
43257. .43288
                                                                                                 .2750 of consensus'
                                                                                                                                                    .168 of consensus"
                                                                                                                                                                                                                                                        .189 of consensus"
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                                                                                                                                                                                                   .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                  .311 of consensus"
                                                                                                                                                                                                                                                                                                                                 35098. .35173
//note="Milk repeat: matches 59. .145 of consensus" 35418. .35735
/note="AluSq repeat: matches 4. .311 of consensus 36438. .36483
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Catarrhini; Hominidae; Homo.
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81;
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7.00te="11 copies 4 mer gaga 81% conserved"

7.00fe="12" copies 4 mer gaga 81% conserved"

7.00te="MLTIC repeat: matches 1. 466 of co

37163. 37465
                                               /note="8 copies 4 mer gtgt 87% conserved"
32209. .3227
/note="L2 repeat: matches 2702. .2750 of
32281. .3239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="23 copies 2 mer ga 80% conserved"
                                                                                                                                                                                32367. .32477
/note="MMR repeat: matches 148.
34251. .34437
/note="MERSA repeat: matches 1.
34326. .34719
                                                                                                                                                 /note="MIR repeat: matches 110.
32367. .32477
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35098. .35173
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Mammalia; Eutheria; Primates;
1 (bases 1 to 126232)
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                                                                                    5486. .5516 of consensus"
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/note="MERS8A repeat: matches 80. .214 of consensus"
33507. .33646
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Anote-"L2 repeat: matches 2256. .2732 of consensus"
33063. .33253
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/note="Alusx repeat: matches 1. .292 of consensus" 26329. .27019
/note="MIR repeat: matches 80. .177 of consensus" 27069. .27349
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33254. .33479
//note="AluX repeat: matches 76. .299 of consensus"
9428. .9461
//note="MRR repeat: matches 158. .192 of consensus"
10349. .10379
/note="LIM3 repeat: matches 5486. .5516 of consensus"
/note="MRR repeat: matches 121. .262 of consensus"
/note="MRR repeat: matches 121. .262 of consensus"
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/note="MIR repeat: matches 61. .250 of consensus"
24244
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Direct Submission
Submitted (09-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waitham, MA 02433, USA
On Jul 17, 2001 Lis sequence version replaced gi:14277218.
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Smith, D.R.
                                                   //note="LiPB1 repeat: matches 5951. .6155 of consensus" 35780. .35827
/note="MIR repeat: matches 103. .151 of consensus" 36408. .36552
/note="Mir repeat: matches 6. .144 of consensus" 36553. .37105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Therapeutics Corporation Sequencing Center: Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / note="MIR repeat: matches 16. .251 of consensus" 38921. .39105
/ note="MIR repeat: matches 13. .200 of consensus" 39331 .39400 s. metches 13. .200 of consensus" 39331 .39400 s. met ac 67% conserved" / note="MERSB repeat: matches 1. .83 of consensus" / note="MERSB repeat: matches 1. .83 of consensus" / note="MERSB repeat: matches 1. .41 of consensus" / note="MERSB repeat: matches 27. .214 of consensus" / 141207 .41379 / note="MIR repeat: matches 27. .214 of consensus" / 1836 .42384
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                                                                                                                                                                                                                                                          /note="MCR41A repeat: matches 1. .554 of consensus" 37106. .37394 /note="MLTIC repeat: matches 144. .458 of consensus" 38198. .38233 /note="E copies 6 mer tgtgtg 97% conserved" 38693. .38883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43433. 43799
forte="THETC repeat: matches 1. .370 of consensus"
forte="THETC repeat: matches 3. .248 of consensus"
forte="MIR repeat: matches 3. .248 of consensus"
forte="MIR repeat: matches 25. .151 of consensus"
forte="MIR repeat: matches 25. .
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Center: Genome Therapeutics Corperation
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repeat: matches
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Smith, D.R.
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AUTHORS
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                                                                                                                                   SOURCE
                                                                                            Sequencing vector: N/A
Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap: version 990315
Consensus quality: 167296 bases at least Q40
Consensus quality: 167296 bases at least Q30
Consensus quality: 168175 bases at least Q20
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                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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                          Web site: http://www.genomecorp.com/
Contact: gtc-segcenter@genomecorp.com
                                                                                                                                                                                                                                                                                                                                                                                                                                         245: contig of 2645 bp in length 2745: gap of unknown length 2746: 13085: contig of 10340 bp in length 13086: contig of 10340 bp in length 1386: 30534: contig of 17349 bp in length 2555 51303: contig of 17349 bp in length 2555 51303: contig of 20669 bp in length 25103: contig of 20669 bp in length 2540: 51403: gap of unknown length 2565 114411: contig of 29761 bp in length 2565 114411: contig of 38147 bp in length 2565 115338: contig of 38147 bp in length 2565 115338: contig of 52527 bp in length 2565 172038: contig of 52527 bp in length.
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/note="assembly_name:Contig5"
| 13186. .3053
/note="assembly_name:Contig6"
| 30635. .51303
/note="assembly_name:Contig7
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/note="assembly_name:Contig8"
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35761 c 34480 g 51423 t
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/organism="Homo sapiens"
/db_xref='taxon:9606"
/chromosome="10"
/clone="RP11-178G16"
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1, .2645
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RESULT

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Assembly program: Phrap; version 990315
Consensus quality: 194541 bases at least Q40
Consensus quality: 195396 bases at least Q30
Consensus quality: 195736 bases at least Q20
Insert size: 198807; sum-of-contigs
Quality coverage: 7.4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submission Cenome Therapeutics Corporation, 100 Beaver Submitted (20 MAY-2001) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA On Jun 7, 2001 this sequence version replaced g1:14290382.
                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 199008)
Smith.D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: N/A Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                Genome Therapeutics Corporation Sequencing Center: Human Genome
HTG 07-JUN-2001
Homo sapiens chromosome 10 clone RP11-296D9, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Genome Therapeutics Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: GTC
Web site: http://www.genomecorp.com/
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2660: gap of unknown length
6272: contig of 3612 bp in length
6372: gap of unknown length
11483: contig of 5111 bp in length
11583: gap of unknown length
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gap of unknown length
contig of 7498 bp in length
                                                                                                                   ACO91699.5 GI:14327753
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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/clone="RP1-296D9"
/clone_lib="RPCI-11"
1. .2560
/note="assembly_name:Contig16"
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/organism≂"Homo sapiens"
/db_xref="taxon:9606"
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1. 199008
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Smith, D.R.
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35393:
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1115)

Mayer,K., Wolff,E., Clevers,H. and Ballhausen,W.G.

The human high mobility group (HWG)-box transcription factor TCF-1: novel isoforms due to alternative splicing and usage of a new exon
                                                                            ris-HCl, pH 9.0 2 ml 100 mM
on X-100 200 ul 1.0 %
gCl2 150 ul 1.0 %
150 ml 15 mM
1 . 25 ml.
Location/Qualifiers
1 . .251
//documentsm="Homo sapiens"
//db_xref="taxon:9606"
//clone_lib="Miscellaneous Y sequences"
//note="Human STSS derived from miscellaneous Y sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="TCF-]"
/gendard_name="T cell factor 1 splice form D"
/standard_name="T cell factor 1 splice form D"
/citation=[1]
/function="high mobility group box transcription factor"
                                                 Final Conc. of 10x Stock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSTCFID 1115 bp mRNA PRI 09-JAN-1995
H.sapiens TCF-1 mRNA for T cell factor 1 splice form D.
247361
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished

(Dases I to 1115)

van de Wetering, M., Oosterwegel, M., Holsteye, F., Dooyes, D., Suijkebuik, K., Geurts van Kessel, A. and Clevers, H.

The human T cell transcription factor-1 gene. Structure, Jocalization, and promoter characterization

J. Biol. Chem. 267 (12), 8530-8536 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                           Length 251;
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                                                                   500 mM
100 mM
1.0 %
15 mM
                                                                                                                                                                                                                                                                                                                                                                                     Score 16.4; DB 11;
Pred. No. 5.9e+02;
); Mismatches 1;
                                                 Volume Mixed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db.xref="taxon:9606"
/Lissue_type="lymphoma"
/cell_type="T-!ymphocyte"
/cell_line="Jurkat"
                              For 20ml of 10x Stock solution:
Stock Reagent Volume Mixe
1M KCi
1M Tris-HCl, pH 9.0 2 ml
Triton X-100 200 ul
2M MGCl2 150 ul
                                                                                                                                                                                                                                                                                                                      45
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65 g
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splice form D; T cell factor 1.
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58 c 6
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Ballhausen, W.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G66013 251 bp DNA STS 01-AUG-2001
sY890 Miscellaneous Y sequences Homo sapiens STS genomic, sequence
tagged site.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 251)
Tilford, C.A., Kuroda-Kawaguchi, T., Skaletsky, H., Rozen, S.,
Brown, L.G., Rosenberg, M., McPherson, J.D., Wylie, K., Sekhon, M.,
Kucaba, T.A., Naterston, R.H. and Page, D.C.
The human Y chromosome: A mosaic of gene-laden amplicons and
**Nomologous domains
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Primer A: CGAGGTGGATAATTTG
Primer B: TTTTTCGTTGGATGATTTG
PCR Profile: 244
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.4%; Score 17; DB 2; Length 199008; Best Local Similarity 100.0%; Pred. No. 73; Matches 17; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                        801 others
                                               G173. .11483

/note="assembly_name:Contig18"

11584. .17593

/note="assembly_name:Contig19"

17694. .25191

/note="assembly_name:Contig20"

25292. .35393

/note="assembly_name:Contig21"

35494. .62376

/note="assembly_name:Contig22"

62477. .103800
                                                                                                                                                                                                                                                                  2661. .6272
/note="assembly_name:Contig17
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each 100 uM
0.05 units/ul
15 ul or 20 ul
15 ul
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1:00 sec
1:00 min
1:00 min
5:00 min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synonyms: PRKY
Contact: Tomoko Kawaguchi
Page Lab
                                      clone_end:T7"
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Homo sapiens
Homo sapiens
Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini: Hominidae: Homo.
1 (bases 1 to 1254)
van de Wetering, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht, The Netherlands
/function="high mobility group box transcription factor"
/evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases I to 1254)
van de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H. Identification and cloning of TCF-1, a T lymphocyle-specific transcription factor containing a sequence-specific HMG box 91114695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSTCF1A 1254 bp mRNA PRI 14-JUN-1
Human TCF-1 mRNA for T cell factor 1 (splice form A).
X59869 X55327 X578785
DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
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422 c 286 g 178 t
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Pred. No. 4.38+02;
0; Mismatches 1; Indels 0;
                                                                                                 /standard_name="T cell factor 1 splice form/citation=[1]
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T lymphocyte"
/cell_line="Jurkat"
/clone_lib="cDNA"
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                                                                                                                                                                                                                                                                                                                                                               /gene="TCF-1"
                                                                 /gene="TCF-1"
2. .1144
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94.48;
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Best Local Similarity 94.4
Matches 17; Conservative
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HSTCF1A/C
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                                                                                                                                                            /product="T_cell factor 1 splice form D"
/product="T_cell factor 1 splice form D"
/protein_id="CAA87439.1"
/d_xxef="G1:619882.1"
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LSLYEHFNSPHPTPAPADISQKQVHRPLQTPDLSGFYSLTSGRAQLPHYSWFTHRS
LMGGGVPGRPAIPHYSWFTHRS
LMLGSGVPGRPAIPHYSWFTHRS
FMLYMKEMRAKUJAGCTLKESAAINOILGREWHALSREEOAKYYELARKEROLHWQLY
PGWSARDNYGKKKRRSREKHQESTTDNSLHYS"
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1 (bases 1 to 1165)

Mayer,K., Wolff,E., Clevers,H. and Ballhausen,W.G.

The human high mobility group (HMG)-box transcription factor TCF-1: novel isoforms due to alternative splicing and usage of a new exon
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Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSTCFIE 1165 bp mRNA PRI 09-JAN-1995
H.sapiens TCF-1 mRNA for T cell factor 1 splice form E.
247362
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van de Wetering,M., Oosterwegel,M., Holstege,F., Dooyes,D.
suijkerbuijk,R., Geurts van Kessel,A. and Clevers,H.
The human T cell transcription factor-1 gene. Structure,
J. Biol. chem. 267 (12), 8530-8536 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.4; DB 9; Length 1115;
Pred. No. 4.3e+02;
0; Mismatches 1; Indels 0
                                                                                                           /standard_name="T cell factor 1 splice form /citation=[1] /codon_start=1
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="lymphoma"
/cell_type="T-lymphocyte"
/cell_line="Jurkat"
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splice form E; T cell factor 1.
                              /evidence=experimental
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                                                            /gene="TCF-1"
2. 754
                                                                                                 /gene="TCF-1"
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Ballhausen, W.G.
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Gaps

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/translation="MYKETVYSAFNLLMHYPPPSGAGGHPOPOPPLKANOPPHGVPO
LALZYBENGRHPAPARADISOKOVHRPUQPPDLSGYFYSLTGSGRGOLPHTYSMFTHPS
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FMLYMKEMRAKVIAECTLKESAAINOILGRRWHALSREEQAKYFELARKEROLHMQLY
GGGARDNYGKKKRRSREKHQESTTETNWPRELKDGNGOESLSMSSSSSPA"
/gene="TCF-1"
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1 (bases 1 to 2814)
van de Wetering,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28 MAY-1991) M. Van De Wetering, Dept of Clinical
Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,
The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Human TCF-1 mRNA for T cell factor 1 (splice form B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .X59870.1 GI:36787
DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
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                                                                                                                                                                                                                                                                                                                                                    91.1%; Score 16.4; DB 9; Length 1254; 94.4%; Pred. No. 4.2e+02;
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/db_xref="SWISS-PROT:P36402"
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/db_xref="SMISS-PROT:p36402"
                                                                                                                                                                                                                                                              /note="alternative splice site"
391 c 335 g 208 t
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/evidence=experimental
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Location/Qualifiers
                                                                                                                                                                                                            /note="HMG box"
                                                                                                                                                                                                                                            /gene="TCF-1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van de Wetering,M., Castrop,J., Korinek,V. and Clevers,H.
Extensive alternative splicing and dual promoter usage generate
Tcf-1 protein isoforms with differential transcription control
                                                                                                                                                                                                                                                                                                                                          Gaps
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Van de Wetering,M.L.

Direct Submission
Submitted (07-JAN-1992) M.L. Van De Wetering, Department of
Immunology, P.O. Box 8550, 3508 GA Utrecht, THE NETHERLANDS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 2855)
Suijkerbuijk, Wolterwegel, M., Holstage, F., Dooyes, D. Suijkerbuijk, W., Gosterwegel, M., Holstage, F., Dooyes, D. Suijkerbuijk, W., Geurts van Kessel, A. and Clevers, H. The human T cell transcription factor 1 gene. Structure, J. Biol. Chem. 267 (12), 8530-8536 (1992)
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1691. .1798,1843. .1890,2054. .2134)
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T-cell transcription factor; transcription factor.
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831 c 648 g 572
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/note="HMG box"
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X63901
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Gaps
Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box EMBO J. 10 (1), 123-132 (1991) 91114695 See also X59869-X59871.
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Pred. No. 3.6e+02;
); Mismatches 1;
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860 c 671 g 597
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80. .886
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94.48;
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Matches 17; Conservative
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    LMLGSGVPGHPAAIPHPAIVPPSGKQELQPFDRNI.KTQAESKAEKEAKKPTIKKPLNA
FMLYMEBMRAKVIARCTILKESAAINGILGBRWHALISPEEDAKYYELLARKERQLHMQLY
PGWLYMEBARNYGKKRRSREKHQESTTETNWPRELKEGNGGESI.SMSSSSPA"
Join (829. 224,970. 1074,1120. 1209,1255. 1374,1420. 1581,
1691. 1798,1843. 1890,2054. 2134)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht, The Netherlands 2 (bases 1 to 2910) van de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
I (bases 1 to 2910)
van de Metering, M.
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ilarity 94.4%; Pred. No. 3.6e+02;
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929 c
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2054. .213
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New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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42.408 Million cell updates/sec
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                                                                            February 20, 2002, 10:32:01; Search time 363.89 Seconds
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| SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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AAC93454
AAH18649
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Maximum Match 100%
Listing first 45 summaries
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                                                       - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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AAD05450
AAH17150
AAH13852
AAC59710
           AAX57478

AAV83941

AAV83942

AAI63452

AAI6448

AAC13252

AAC13252

AAC13252

AAC13253

AAC13253

AAC13253

AAC13253

AAC15264

AAC17237

AAC17237
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AAC14388/c
ID AAC14388 standard; CDNA; 227
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             06-OCT-2000 (first entry)
             Dumas Milne Edwards J,
                                                                                        (GEST ) GENSET.
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           The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different Lissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet heen conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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to 5'ESTs and for
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                                                                                                                                                                                                                                                                                                                                                  Score 15.4; DF
Pred. No. 97;
0; Mismatches
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                                                                                                                                                                                                                                                         expression and secretion vectors.
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94.1%;
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Best Local Similarity 94.1'
Matches 16; Conservative
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gene therapy;
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                 in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules encoding 48 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives \cdot
                                                                                                                                                                                                       Gaps
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                                                                                                                                                              DB 21; Length 244;
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                                                                                                  66 T; 0 other;
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                                                                                                                                                            Score 15.4; DB Pred. No. 98; 0; Mismatches
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                                                                                                    Sequence 244 BP; 62 A; 57 C; 59 G;
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                                                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                              85.6%;
94.1%;
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                                                                                                                                                                                                                                                                                    104 ccgaggtgggttgggtca 120
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                                                                                                                                                                                                                                           l ccgaggtgggtgggtaa 17
                                                                                                                                                              Query Match 85.6
Best Local Similarity 94.1
Matches 16; Conservative
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P-PSDB; AAB51762.
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e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotais. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. Oligonucleotide AAC93413 - AAC93421 and peptide AAB51723 are used in the isolation and characterisation of the proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs -
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Otsuki T;
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Wakamatsu A, Nagai K,
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Pred. No. 1e+02;
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2000JP-0118776.
2000JP-0183767.
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ilarity 94.1%;
Conservative
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27-AUG-1999;
11-JAN-2000;
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complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a complementary configuration comprises a 3'-end sequence, where the complementary to a coligonucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the checking and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the chill-length cDNAs. The primers and sequences and the full-length cDNAs as easily without any specialised methods. AAM932446 to AAM13633 to AAM936893 represent human cDNA sequences; and AAM13629 to AAM13632 of the protein exemplification of the process the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an ollgo-dT primer and an ollgonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Otsuki
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T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    le+02;
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Pred. No. 1e+02
0; Mismatches
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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94.1%;
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Best Local Similarity 94.1
Matches 16, Conservative
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02-MAY-2000;
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oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the comprising a sequence comprises a 5'-end sequence and an oligonucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence, where the polynucleotide comprises a 3'-end sequence, where the comprises a 1 least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs asally without any specialised methods. AAH03166 to AAH13638 and AAH13633 to AAH18631 crepresent human cDNA sequences; and AAH13632 to AAH13632 trepresent human amino acid sequences; and AAH13639 to AAH13632 trepresent invention.
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                                                                                                                                                                                                                                                                                                                           Gaps
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/note= "Coding region is interrupted with introns"
/tage b
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                                                                                                                                                                                                                                                                                             85.6%; Score 15.4; DB 22; Length 4372; 94.1%; Pred. No. 1.1e+02; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                        Sequence 4372 BP; 1270 A; 862 C; 1032 G; 1208 T; 0 other;
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289..1280
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1581..1819
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1820..1855
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1856..2466
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Matches 16; Conservative
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The present sequence is the genomic DNA encoding CD39-14 protein, an apyrase and/or nucleotide diphosphates (NDPase). It is isolated from the human CITB BAC genomic library. It is a soluble ATP Diphosphoydrolases (ATPDase) and is involved in the hydrolysis of adenosine diphosphate (ADP), the agonist that causes platelet aggregation. CD39-14 protein has 30% and 80% homology to human and murine CD39. It has platelet aggregation inhibition and antithrombotic activity. CD39-14 is used to treat or prevent thrombosis, mycocardial infarction, cerebral ischemaia and angina. It is also used in vitro, to maintain vascular grafts or during extracorporeal circulation, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid encoding human CD39-like protein, useful for treating preventing thrombotic disease .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Page 112-119; 125pp; English.
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98US-0122449.
99US-0244444.
99US-0273447.
99US-0350836.
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5988..6965
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3951..4893
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4996..5846
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2556..2862
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24-JUL-1998;
04-FEB-1999;
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09-JUL-1999
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hydrolyse NDP, as molecular weight markers and as nutritional supplements. It is used to identify therapeutic agents that bind and modulate CD39-L4. It is coupled to toxins for targeting drugs to tumours or other cells that express CD39-L4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myocardial infarction; cerebral ischaemia; angina; arterial thrombosis; cerebral artery thrombosis; platelet aggregation; inflammation; apoptosis; autoimmune discorder; neurological disorder; Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotides encoding human CD39-like polypeptides, with apyrase and/or NDPase activity, which are useful in the treatment of pathological conditions caused by thrombosis (e.g. myocardial
                                                                                                                                                                    0;
                                                                                                                                   Length 9365;
                                                                                 Sequence 9365 BP; 2439 A; 2005 C; 2191 G; 2632 T; 98 other;
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Human CD39 like protein CD39-L4 partial DNA sequence.
                                                                                                                                 Score 15.4; DB 21;
Pred. No. 1.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infarction) and inflammatory disorders -
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                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-0481238.
; 2000US-0557800.
; 2000US-0583231.
; 2000US-0608285.
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                                                                                                                                   85.68;
                                                                                                                                 Query Match 85.6%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                     3219 ccgaggtgggtgggtca 3235
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                                                                                                                                                                                                    1 ccgaggtgggtgggtaa 17
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CD39-like protein; apyrase; NDPase; platelet function inhibitor; myocardial infarction; cerebral ischaemia; angina; arterial thrombosis; cerebral arterial thrombosis; appoptosis; platelet aggregation; inflammation; appoptosis; autoimmune disorder; neurological disorder; Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ds.
disorders involving sepsis or systemic inflammatory response syndrome care associated conditions such as fever, tachycardia, tachypnea, cytokine overstimulation); autoimmune disorders such as thrombosis, atherosclerosis, acute pancreatitis, dermatitis, including psoriasis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis; and cancer. The present sequence represents a CD39 like protein CD39-L4 partial DNA sequence.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                               Length 9365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotides encoding human CD39-like polypeptides, with an and/Or NDRapes activity, which are uscful in the treatment of pathological conditions caused by thrombosis (e.g. myocardial infarction) and inflammatory disorders
                                                                                                                                                                                                       Sequence 9365 BP; 2439 A; 2005 C; 2191 G; 2632 T; 98 other;
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                                                                                                                                                                                                                                                               Score 15.4; DB 22;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                        0; Mismatches
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2000US-0481238.
2000US-0557800.
2000US-0583231.
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16; Conservative
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25-APR-2000;
26-MAY-2000;
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Best Local S
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with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are userua and apoptosis) associated with ADP or other purinergic signalling by reducing the levels of NDPs. The polypeptides are also useful for prophylaxis or treatment of inflammation related disorders, such as disorders involving sepsis or systemic inflammatory response syndrome or SIRS (and associated conditions such as fever, tachycardia, tachypnea, cytokine overstimulation); autoimmure disorders such as thrombosis, atherosclerosis, acute pancreatitis, dermatitis, including psoriasis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, neurological disorders including neurodegenerative diseases, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CD39-like protein, apyrase; NDPase; platelet function inhibitor; myocardial infarction; cerebral ischaemia; angina; arterial thrombosis; cerebral artery thrombosis; platelet aggregation; inflammation; apoptosis; autoimmune disorder; neurological disorder; Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ds.
                                                                                                                                                                                                                                                              sequence represents the CD39 like protein CD39-L4 genomic DNA sequence.
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                                                                                                                                                                                                                      depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis; and cancer. The present
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                                                                                                                                                                                                                                                                                                  Sequence 14747 BP; 3821 A; 3235 C; 3349 G; 4294 T; 48 other;
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11.-JAN-2000; 2000US-0481238.
25-APR-2000; 2000US-0557800.
26-MAY-2000; 2000US-0583231.
30-JUN-2000; 2000US-0608285.
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                                                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
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Best Local Similarity
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c function and can therefore be used in the prophylaxis or treatment of pathological conditions caused by or involving thrombosis or excessive coagulation or excessive platelet aggregation, such as myocardial coagulation or excessive platelet aggregation, such as myocardial coagulation, cerebral ischaemia, angina, arterial thrombosis, cerebral artery thrombosis or intracardiac thrombosis, and conditions associated with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in modulating disease states (including platelet aggregation, inflammation and apoptosis) associated with ADP or other purinergic signalling by reducing the levels of NDPs. The polypeptides are also useful for prophylaxis or treatment of inflammation related disorders, such as disorders involving sepais or systemic inflammatory response syndrome or SIRS (and associated conditions such as fever, tachycardia, tachypnea, cytokine overstimulation); autoimmune disorders such as thrombosis, attentions, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, multiple sclerosis, arthritis; capenses, and amyotrophic lateral sclerosis; and cancer. The present cycle sequence represents the CD39 like protein CD39-L4 genomic DNA sequence.
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Pred. No. 1.1e+02;
); Mismatches 1;
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2000US-019874
2000US-0198174
2000US-0198123
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2000US-0224518.
2000US-0224519.
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2000US-0184664.
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04-FEB-2000;
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11-JUL-2000;
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14-AUG-2000;
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14-AUG-2000;

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2000US - 0225214.
2000US - 0225214.
2000US - 0225267.
2000US - 0225268.
2000US - 0225447.
2000US - 0225470.
2000US - 0225770.
2000US - 0225779.
2000US - 0225779.
2000US - 0225779.
2000US - 022688.
2000US - 0229287.
2000US - 0229287.
2000US - 0229287.
2000US - 0229344.
2000US - 0229344.
2000US - 0229347.
2000US - 0229347.
2000US - 0229348.
2000US - 0229389.
2000US - 0229399.
2000US - 023299.
2000US - 0233896.
2000US - 0236802.
2000US - 0236802.
2000US - 0236902.
2000US - 0236902.
2000US - 0236902.
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2000US-0239935.
2000US-0239937.
2000US-0240960.
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2000US-0246477.
2000US-0246477.
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2000US-0241785.
2000US-0241786.
2000US-0241786.
                                 14-Aug-2000; 2

15-Aug-2000; 2

16-Aug-2000; 2

17-Aug-2000; 2

18-Aug-2000; 2

18-Aug-2000; 2

18-Aug-2000; 2

19-SEP-2000; 2

10-SEP-2000; 2

11-SEP-2000; 2
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of a number of ovarian and breast antigens. These are shown in AAI62467-AAI62572 and AAM422440-AAM42345. The sequences can be used in t diagnosis, prevention and treatment of breast and ovarian cancers, and their metastases. The present sequence is a genomic sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 16225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16225 BP; 4434 A; 3583 C; 3702 G; 4506 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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85.6%; Score 15.4; DB 22;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM;
08-NOY-2000; 2000US-0246523.
08-NOY-2000; 2000US-0246524.
08-NOY-2000; 2000US-0246526.
08-NOY-2000; 2000US-0246528.
08-NOY-2000; 2000US-0246528.
08-NOY-2000; 2000US-0246528.
08-NOY-2000; 2000US-0246528.
08-NOY-2000; 2000US-0246611.
08-NOY-2000; 2000US-0246611.
08-NOY-2000; 2000US-0249209.
17-NOY-2000; 2000US-0249209.
17-NOY-2000; 2000US-0249209.
17-NOY-2000; 2000US-0249211.
17-NOY-2000; 2000US-0249211.
17-NOY-2000; 2000US-0249211.
17-NOY-2000; 2000US-0249218.
17-NOY-2000; 2000US-0249285.
17-NOY-2000; 2000US-0249286.
17-NOY-2000; 2000US-0249288.
01-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251989.
06-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488785/53.
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23-SEP-1999

AAX90201;

AAX90201

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Homo sapiens WO9935290-A1. 07-JAN-1999; 08-JAN-1998;

15-JUL-1999.

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This invention describes novel rat-derived nucleic acid fragments from cellular genes that are necessary for viral infection but not for cell survival, or that suppress tumour progression. The products of the invention (AAX5737-X57497) can be used in methods of identifying cellular genes necessary for viral growth and cellular genes that function as tumour suppressors and for reducing or preventing such infections or cancer. They may also be used in screening for potential therapeutic agents. These sequences can be targeted without significant side effects (contrast targeting genes essential for viral growth).
                                                                                                                                                                                      Gene trap; rat; cellular gene; viral infection; cell survival; cancer; tumour progression; suppression; identification; viral growth; tumour suppressor; prevention; screening; therapeutic agent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; neocentromere; replication; extra-chromosomal element; septegation; cell division; artificial chromosome; gene therapy; BAC; transgenic; human artificial chromosome; bacterial artificial chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding tumor suppressors and products required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1072 BP; 251 A; 235 C; 298 G; 241 T; 47 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial artificial chromosome (BAC)-F2 contig 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83,3%; Score 15; DB 20; 1100,0%; Pred. No. 1.6e+02;
                                                                                                                                               Rat U3 gene trap derived nucleic acid 31_4_2-rE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 85; 94pp; English.
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AAV83941/C
ID AAV83941 standard; DNA; 5596 BP.
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AAX57478/c
ID AAX57478 standard; DNA; 1072 BP.
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Best Local Similarity 100.
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Organ EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-326546/27.
                                                                                                                                                                                                                                                                                              Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viral infection
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                                                                                                                                                                                                                                                                                                                                          W09919481-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1999
                                                                                                             24-JUL-1999
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                                                                    AAX57478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for detecting a genetic mutation in the yes1 gene for the diagnosis of a yes1 mediated nutation in the yes1 gene for the diagnosis of a yes1 mediated neuropsychiatric disorder in a human. The method comprises detecting the presence or absence of a genetic mutation in the yes1 gene of the subject, where the genetic mutation is a substitution, insertion or a detection and results in the production of a yes1 protein having an amino acid sequence other than the wild-type yes1 amino acid sequence and the presence of the genetic mutation identifies a subject that has or is at presence of the yes1 protein, aller the amount of the protein, or alter that bind to the yes1 protein, alter the amount of the protein, or alter the activity of the yes1 gene product, are useful for treating a yes1 mediated neuropsychiatric disorder. Compounds considered neuropsychiatric disorder (BAD) also known as bipolar mood disorder (BP) or manic-depressive illuses. The method distinguishes neuropsychiatric disorders from contrological disorders, which enables more accurate evaluation and present treatment. The present sequence represents the human yes1 cDNA sequence.
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                                                                                                                                                                                                                                                                                                                      Human; yes1; diagnosis; neuropsychiatric disorder; BAD; schizophrenia; bipolar affective disorder; attention deficit disorder; schizoaffective disorder; unipolar affective disorder; Huntington's disease; Parkinson's disease; manic-depression; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of a genetic mutation in the yes! gene, useful for diagnosis of a yes! mediated neuropsychiatric disorder in a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 119950 BP; 34471 A; 23730 C; 24660 G; 37033 T; 56 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.4; DB 20; Length 119950;
Pred. No. 1.2e+02;
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                                                                                                                                               AAX90201 standard; DNA; 119950 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC.
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94.1%;
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              8511 CCGAGGTGGGTGATAA 8495
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                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 94.1
Matches 16; Conservative
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P-PSDB; AAY24421.
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Gaps

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Length 1072; Indels

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97AU-0008791.
97AU-0006784.
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           26-AUG-1997;
13-MAY-1997;
                                                                                                       Cancilla MR,
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                                                                                                                                                                                                                                     therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a bacterial artificial chromosome (BAC) contig, and exemplifies the invention. The specification describes contig, and exemplifies the invention. The specification describes nucleic acid sequences derived from a eukaryotic chromosoume, including a necentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during during during for use in gene therapy comprising a replicable, segregating uncleic acid that confers a specific phenotype on cells. Human artificial chromosomes can propagate in human cells and extra-chromosomal, they are not mutagenic. The artificial chromosomes carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes carry large amounts of content mutagenic reagents, e.g. for production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to increase the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes.
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                                                                                                                                                                                                                                                                    New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5596 BP; 1730 A; 1019 C; 1082 G; 1763 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NC-contig derived from mardel(10) on chromosome 10q25.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%; Score 15; DB 20; I
100.0%; Pred. No. 1.7e+02;
Tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 177-181; 540pp; English.
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ID AAV83940 standard; DNA; 80240 BP.
                                                                                                                                                              (AMRA-) AMRAD OPERATIONS PTY LID.
                                                                                                                           97AU-0006784.
                                                                    98WO-AU00352.
                                                                                                         97AU-0008791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 83.3
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                 Choo K,
                                                                                                                                                                                                                                   WPI; 1999-009773/01.
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                                                                                                                                                                                                 Cancilla MR,
                                                                      13-MAY-1998;
                                                                                                         26-AUG-1997;
                                                                                                                           13-MAY-1997;
WO9851790-A1
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                                   19-NOV-1998.
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The present sequence represents the NC-contig derived from a mutated human chromosome 10, 10425. 2 region. The sequence contains and chromosome 10, 10425. 2 region. The sequence contains a functional marker referred to as mardel(10). The mardel(10) marker is mitotically stable and contains a functional marker is mitotically stable and contains a functional neocentromere at a location regarded as non-centromeric. This neocentromere maps to q25.2 on chromosome 10. The specification describes nucleic acid sequences derived from a eukaryotic chromosome, including a neocentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype on cells. Human artificial chromosomes can propagate in human cells and carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes can a an analys, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antipoliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; antiallergic; hepatotropic; antidiabetic; antidiametory; antiuleer; vulnerary; anticonvulsant; antiparasitlic; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to increase the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                           New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome – used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 80240 BP; 23102 A; 16537 C; 16747 G; 23846 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human kidney related polynucleotide SEQ ID NO 767.
                                                                                                Du Sart D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Fig 16A; 540pp; English.
(AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA163452 standard; DNA; 115 BP.
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Best Local Similarity 100.
Matches 15; Conservative
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001WO-US0134; 000US-0179065 000US-018062 000US-018635 000US-018635 000US-018635	2000US-0229467. 2000US-0214886. 2000US-0215135. 2000US-0215886. 2000US-0215880. 2000US-0217486. 2000US-0217486. 2000US-021890. 2000US-022804. 2000US-022824. 2000US-0228266. 2000US-0228266. 2000US-0228266. 2000US-0228266. 2000US-0228266. 2000US-0228266. 2000US-0228266. 2000US-0228266. 2000US-0228268. 2000US-0228268. 2000US-0228289. 2000US-0228943.	0001S-0231414 0001S-0231414 0001S-0232081 0001S-0232391 0001S-0232391 0001S-0232391 0001S-0232390 0001S-0232401 0001S-0233063 0001S-0233063 0001S-0233063 0001S-0233063 0001S-0233063 0001S-0233063 0001S-023363 0001S-023363
7-JAN-2001 1-JAN-2000 4-FEB-2000 2-MAR-2000 6-MAR-2000 6-MAR-2000	A X Z L L L L L L L L L L L L L L L L L L	
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The invention relates to novel kidney related polynucleotides

(AAI62971-AAI63793) and the encoded polypeptides (AAM42417-AAM42691)

(Collectively known as kidney antigens and the use of such kidney antigens

(Collecting) known as kidney antigens and the use of such kidney antigens

(Collecting) the kidney, cancer and

(Collecting) treventing, treating or amellorating medical conditions

(Collecting) antibodies and (anti) agonists are useful in the diagnosis.

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(Collecting) antibodies and (anti) agonists are useful in the diagnosis.

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(Collecting) antipodies and antipodies and antipodies.

(Collecting) antipodies and diseases e.g. cerebral anoxia and epilepsy:
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders \,
                                                                               Disclosure; SEQ ID NO 767; 564pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 115 BP; 28 A; 27 C; 35 G; 25 T; 0 other;
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Search completed: February 20, 2002, 10:32:12 Job time: 10240 sec

0

Gaps

0;

Ouery Match 82.2%; Score 14.8; DB 22; Length 115; Best Local Similarity 88.9%; Pred. No. 1.9e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0;

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113, App 17, Appl 1, Appli 1, Appli 1, Appli

Sequence

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Sequence Sequence

19, Appl 15, Appl 69, Appl

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Sequence 2, Application US/09103840A
| Patent No. 6294328
| General Discention US/09103840A
| Patent No. 6294328
| General Discention US/09103840A
| General Discention US/09103840A
| APPLICANT: FlactSCHMAN, Robert D.
| APPLICANT: FlactSCHMAN, Robert D.
| APPLICANT: FlactSCHMAN, Robert D.
| APPLICANT: PRASER, Claire M.
| APPLICANT: PRASER, Claire M.
| APPLICANT: PRESER, Claire M.
| TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: US/09/103,840A
| CURRENT APPLICATION NUMBER: US/09/103,840A
| CURRENT FILING DATE: 1998-06-24
| NUMBER OF SEQ ID NOS: 2
| SOFTWARRE: Patentin Ver. 2.1
| SSOFTWARRE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION 1998-06-24
CURRENT PILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: CDC 1551
CTHER INFORMATION: "n" bases at various positions throughout the CTHER INFORMATION: represent a, t, c or 9
US-09-103-840A-2
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Pred. No. 33;
0; Mismatches 1;
US-08-592-126-128
US-08-040-548-32
S206152-8
FOT-US96-10521-19
PCT-US96-10521-15
US-08-935-26-3
PCT-US96-10521-15
US-08-935-26-3
US-08-935-26-3
US-08-935-3
US-08-935-3
US-08-935-3
US-08-935-3
US-08-935-3
US-08-935-3
US-08-832-81-3
US-08-832-81-1
US-08-944-1
US-08-741-1
                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 4325921 CGAGGTGGGTGGGGAAT 4325905
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Best Local Similarity 94.1
Matches 16; Conservative
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1200
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Sequence 5, Appli
Sequence 4, Appli
Sequence 13, Appli
Sequence 3, Appli
Sequence 1, Appli
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                                                                                                                                           Search time 166.82 Seconds (without alignments) 24.437 Million cell updates/sec
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Sequence 3, P
Sequence 3, P
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Sequence 1
Sequence 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*

| 'cgn2_6/ptodate/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodate/2/ina/6B_COMB.seq:*
3: /cgn2_6/ptodate/2/ina/6A_COMB.seq:*
4 /cgn2_6/ptodate/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodate/2/ina/6B_COMB.seq:*
6: /cgn2_6/ptodate/2/ina/perty.comB.seq:*
                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 US-09-103-840A-1

US-09-103-840A-1

US-09-078-294-4

PCT-US95-08295-13

US-09-078-294-4

PCT-US95-08295-13

US-09-385-384-1

US-09-386-384-1

US-08-38-384-1

US-08-312-157-3

US-08-312-157-3

US-08-312-157-3

US-08-312-157-3

US-08-95-7294-10

PCT-US95-07201-10

PCT-US95-07201-10

PCT-US95-07201-10

PCT-US95-07201-10

PCT-US95-07201-10

PCT-US95-07201-10

PCT-US93-096-10

US-08-382-578-5

US-09-081-320-38

US-09-081-320-3

US-09-081-320-3

US-09-081-320-3

US-09-081-320-1

US-08-350-715-1

US-08-850-715-1

US-08-850-715-1
                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                         351203 seqs, 113238999 residues
                                                                                                                                             February 20, 2002, 07:44:50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                            nucleic search, using
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83.3 80246 4 0

83.3 80246 4 0

82.2 2886 3 0

82.2 2686 3 0

82.2 2919 3 0

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82.2 39146 2 0

82.2 27210 5 p

82.2 27210 5 p

82.2 27481 5 p

82.2 27481 5 p

82.2 367481 5 p

80.0 1161 1 0

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80.0 1166 3 0

80.0 6486 3 0

77.8 12847 1 0

76.7 302 2 0
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18
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seq length: 2000000000
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Match Length DB
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Perfect score:
Sequence:
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Maximum DB
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Gaps

Indels

Length 4403765;

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Sequence 3, Application US/09095385
Patent No. 6300104
GABERAL INFORMATION:
APPLICANT: Morrison, Sherie L.
APPLICANT: Chintalacharuvu, Kote R.
TITLE OF INVENTION: BY SINGLE CELLS AND METHODS FOR MAKING AND USING TITLE OF INVENTION: SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Merchant, Gould, Smith, Edell, Welter & Schmidt
11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            BREAST SPECIFIC GENES AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/KISGE *** PCT/KISGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
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APPLICATION NUMBER: US/09/095.385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8; DE
Pred. No. 82;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/09/095,385
09-JUN-1998
                                                                                                                                                                                                                                                                                                                         Sequence 13, Application PC/TUS9508295; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,969
FILING DATE: 19-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Canady, Karen S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-08295-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.2%;
88.9%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ccgaggtgggtgggtaat 18
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                                                                                      Db 70981 AGGTGGGTGGTAAT 70967
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BRE NUMBER OF SEQUENCES: 30 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of the second states o
                                        4 aggtgggtgggtaat 18
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STREET: 11150 Santa
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                             PCT-US95-08295-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-095-385-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Length 5596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REPERRNCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT APPLICATION NUMBER: 1998 05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
SSOFTWARE: 5596
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APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT APPLICATION NUMBER: US/09/078,294
NUMBER OF SEQ ID NOS: 29
SEQ THARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 80246
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Pred. No. 33;
0; Mismatches
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; ORGANISM: Nucleotide sequence of NC-contig
(NC-09-078-294-4
                                                                                                                                                                   TYPE: DNA
ORANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Sequence 4, Application US/09078294
Patent No. 6265211
GENERAL INFORMATION:
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; Patent No. 6265211
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94.18;
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: BAC-F2 contig 1
US-09-078-294-5
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                                                                                                                          LENGTH: 4411529
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US-09-312-157-3/c
US-09-312-157-3/c
Sequence 3, Application US/09312157
Factor No. 6303341
GENERAL INFORMATION:
APPLICANT R. ANDREW C. HTATT, JULIAN
T. ANDREW C. HTATT, JULIAN
T. ANDREW C. HTATT, JULIAN
T. TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTECTION
TITLE OF INVENTION: IMMUNOGLOBULINS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 08/36/395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 212/127
FELECOMMUNICATION INFORMATION:
TELEPAX: (619) 552-8400
TELEX: 67-3510
TELEX: 67-3510
TELEX: 67-3510
TELEX: SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENATH: 2919 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERfect 5.1
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.8; DE
Pred. No. 86;
0; Mismatches
           COMPUTER REDABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURENT APPLICATION DATA:
PELLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.2%;
88.9%;
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2919 base pairs
TYPE: nucleic acid
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Best Local Similarity 88.99
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TOPOLOGY: DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 90071
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APPLICANT: Breat D.
APPLICANT: Breat D. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 1 EXPRESS
THE REPERENCE: RTS-0083
CURRENT APPLICATION NUMBER: US/09/358,384
CURRENT FILING DATE: 1999-07-21
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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88.9%; Pred. No. 86;
Live 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                   82.2%; Score 14.8; DB 4; Length 1839;
88.9%; Pred. No. 85;
Live 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C., MA, THOMAS LEHNER
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
UNMERS OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
REGISTRATION NUMBER: 39,927
REFERENCE/DOCKET NUMBER: 30435.45USU1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
TELEFAX: 310 445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-434-000A-3/c
; Sequence 3, Application US/08434000A
; Patent No. 6046037
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-358-384-1/c; Sequence 1, Application US/09358384; Patent No. 6130088
                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-09-095-385-3
                                                                                                                         INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1839 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1940 CCGAGGTGGGTGGATCAT 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ccgaggtqggtgggtaat 18
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                     Query Match 82.2
Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (16)..(1335)
US-09-358-384-1
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STATE: California
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NAME/KEY: misc_feature; OTHER INFORMATION: /note= "Nucleotides 2272 through 2729 are a coffer INFORMATION: thrombin responsive element"; Human US-08-965-729A-2
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APPLICANT: Ruddy, David A.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Trochihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZOUNTRY: USA
ZIPE: RAJABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: REJABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: S. 35,136
ATORNEY AGRENT INFORMATION:
NAME: Fitts, Renee A.
REFERENCE/DOCKET NUMBER: 35,136
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFARA: 415-576-0200
TELEFAX: 415-576-0300
TELEFAX: 415-576-0300
TELEFAX: A15-576-0300
TELEFAX: A15-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1..3416
OTHER INFORMATION: /note= "cDNA 44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 15, Application US/08724394A; Patent No. 5872237; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feder, John N.
Kronmal, Gregory S.
                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: not relevant
not relevant
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 CCGAGGTGGGTGGATCAT 300
  SEQUENCE CHARACTERISTICS:
LENGTH: 3224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                               1 ccgaggtgggtgggtaat 18
                                                                                                                                                                                                                                                                                                                                    Query Match 82.2
Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polyimmunoglobulin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08965729A
Patent No. 6200751
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jian-Ming Gu and Charles T. Esmon
TITLE OF INVENTION: EMDOTHELIUM SPECIFIC EXPRESSION
TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patea L. Pabst
STREET: 2800 One Aliantic Center, 1201 West Peachlree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 2919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/965,729A
FILING DATE: 07-NOV-1997
FILING DATE: 14-May-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: 08/434,000
ATTORILING DATE: «Unknown»
ATTORILING DATE: «Unknown»
ATTORILING DATE: «Unknown»
NAME: Guise, Jeffrey W.
REFERENCE/DOCKET NUMBER: 31,613
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEPHORE: (619) 552-8400
TELEPHORE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.2%; Score 14.8; D
88.9%; Pred. No. 86;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 235....2472
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coding Sequence 235....2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,718
FILING DATE: 08-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2919 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                            SEQUENCE LISTING
                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMF
TELECOMMUNICATION INFORMATION
TELEPHONE: 404-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ccgaggtgggtgggtaat 18
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 16; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 30309-4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 0'CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-965-729A-2/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-312-157-3
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Gaps

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APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Tainwaki, Takayuki
TITLE OF INVENTION: PIGMENT PEITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
TOWNER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.8; DB 5; Length 7210;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0 kb Not 1-Not
fragment; Derived from human placental
genomic DNA; also referred to as JT106
  Indels
  5
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 07-JUN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REFERENCE/COCKET NUMBER: 20264126PCT
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ 1D NO: 10:
SEQUENCE CHRRACTERISTICS:
FENDENCE CHRRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy Disk
COMPUTER: IMP PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
                                                                                                                                            RESULT 13
PGT-US95-07201-10
PGT-US95-07201-10
GENERAL INFORMATION:
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0
                                                                  Db 1617 CCGAGGTGGGTGGATCAT 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.2%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JUPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                          1 ccgaggtgggtgggtaat 18
                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7210 Base Pairs
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acid
FDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
OTHER INFORMATION: 7.0
OTHER INFORMATION: GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: DASH II
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: JT6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10154
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  16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
  Matches
                                            ò
                                                                                                        0
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PICHENT EPITHELIUM
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : IDENTIFICATION METHOD:
: OTHER INFORMATION: 7.2 kb No. 5840686 l fragments
: OTHER INFORMATION: Derived from human placental genomic DNA
US-08-257-963810
                                                              DB 2; Length 3416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.8; DB 2; Length 7210;
Pred. No. 87;
                                                                                                      2; Indels
                                                            Score 14.8; D
Pred. No. 86;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC COMPATIDLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/257,963B

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20264126US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATONNEY_AGENT INFORMATION:
NAME DONOTHY R AUTH
REGISTRATION NUMBER: 36434
REFERENCE/POCKET NUMBER: 20264126
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LEMOTH: 7210 Base Pairs
TYPE: Nucleic Acid
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                      ; Sequence 10, Application US/08257963B
; Patent No. 5840686
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                            Query Match 82.2%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                Db 3146 CCGAGGTGGGTGGATCAT 3129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.2%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic DNA
                                                                                                                                              1 ccgaggtgggtgggtaat 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: DASH II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: JT106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                              RESULT 12
US-08-257-963B-10
US-08-724-394A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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0

Gaps

0;

Indels

5;

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Search completed: February 20, 2002, 07:51:10 Job time: 578 sec
                           RESULT 15
US-09-301-665-3
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                                                                                                                        PCT-10595-701-43

PCT-10595-701-43

PCT-10595-701-43

Sequence 43, Application PC/TUS9507201

Sequence 43, Application PC/TUS9507201

GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: DERVEW PITTHELIUM
TITLE OF INVENTION: DERVEW FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
CORRESPONDENCES:
ADRESSEE: MATGAN & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IDENTIFICATION METHOD:
; OTHER INFORMATION: full length genomic
; OTHER INFORMATION: sequence for PEDF plus flanking sequences.
PCT-US95-07201-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
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Pred. No. 89;
0; Mismatches
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: FLORPY Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FLILIG DATE: 06-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION NUMBER: 08/257,963
FILING DATE: 24-SEP-1992
ATTORNEY/AGGNT INFORMATION:
 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                 TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 88.3%
Best Local 5. Conservative
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: P1-147
                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
 16;
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
 Matches
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Gaps
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                                                                                                                                               Length 36741;
                                                                                                                                                           Indels
                                                                                                                                                DB 4;
                                                                                                                                               82.2%; Score 14.8; C
88.9%; Pred. No. 89;
iive 0; Mismatches
                                                                                                                                                                      Ouery Match 82.2'
Best Local Similarity 88.9'
Matches 16; Conservative
                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-301-665-3
                                                                                                              36741
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us-09-904-420a-9.rst

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February 20, 2002, 10:25:49; Search time 3814.84 Seconds (without alignments) 50.703 Million cell updates/sec
                                                                                                                                                                                                                                                                              22703874
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                               11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                             US-09-904-420A-9
18
1 ccgaggtgggtgaat 18
                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_esthum:*
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em_esto:*
gb_est:*
gb_est:*
gb_est:*
em_gss_fun:*
em_gss_fun:*
em_gss_pro:*
                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
Sequence:
                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                  Searched:
                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

, Description	AQ744329 HS_5502_A	AA573670 nf42q01.s	AQ217892 HS_2257_B	RG386035 602455204	R35371 HS-1028-B1-	T08252 EST06143 ln	BE940403 RC3-UT006	B33138 HS-1016-B1-	BE723699 193604 MA	B86654 RPCI11-24H2	B73071 RPCI11-11C1	AQ240635 CIT-HSP-2
SUMMARIES	AQ744329	AA573670	AQ217892	BG386035	B35371	T08252	BE940403	B33138	BE723699	B86654	B73071	AQ240635
DB	13	10	13	11	13	11	11	13	10	13	13	13
% Query Match Length DB	617	181	263	353	359	382	399	442	444	455	470	471
% Query Match	94.4	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1
Score	17	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4
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Result No.	υ	Ų		υ	O					υ		

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492 13 AQ322652 598 13 AQ728552 593 13 AQ702852 593 13 AQ706721 8931 11 BF130894 976 11 BF682098 494 11 BF682098 494 11 BF682098 494 11 BF682098 705 11 BF682098 707 11 BF8213792 222 10 AB213792 224 10 AA320156 225 10 AA320156 226 10 AA320156 227 10 AA320156 228 10 AA320197 229 10 AA320197 229 10 AA320197 220 10 BB140909 229 10 BB140909 229 10 BB140909 230 10 BB140909 230 10 BB140909 231 10 BB140909 232 10 BB140909 233 10 BB500836 316 10 BB500836 316 10 BB500836 317 11 FF853474 326 11 FF853474	A0744329 617 bp DNA GSS HS_5502_A2_D04_T7A RPCI-11 Human Male BAC Libr. genomic clone Plate=1078 Col=8 Row=G, DNA sequ. A0744329 A0744329 A0744329 GSS. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalia; Eutheria; Primates; Catarrhini; Homi Lebases 1 to 617) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzo Keller, A., Shaker, R., Furlong, J., Young, J., ZhHood, L. Sequence-tagged connectors: A sequence approac scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9380589 Contact: Mahairas GG, Wallace JC, Hood I, High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109 Tel: (206) 616-3618 Email: jwallacedu. washington.edu Clones are derived from the human BAC library Library availability, please contact Pieter de (pletre Gelejong) med-bulfalo.edu). Clones are derived from the human BAC library Library availability, please contact Pieter de (pletre Gelejong) med-bulfalo.edu). Clones are derived from the human BAC library clones are derived from Luffalo.edu). Clones are derived from Luffalo.edu). Clones may bacter des (pletre Gelejong) med-bulfalo.edu). Clones med-bulfalo.edu Plate: 1078 row: G column: 8 Seq primer: T7
24	A0744329 HS_5502_A2_D04_genomic clone factors in the factor of the facto
	RESULT 1 A0744329/C LOCUS DEFINITION ACCESSION VERSION KEYWORGE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 263)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                          AQ217892 263 bp DNA GSS 19-SEP-1998 HS_2257_B2_C01_T7 CIT Approved Human Genomic Sperm Library D Homo AQ217892 Grome Piate=2257 Co1=2 Row=F, DNA sequence.
PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
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/clone="Plate=2257 Col=2 Row=F"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
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Pred. No. 2.2e+03;
0; Mismatches 1;
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94.4%; Pred. No. 2.1e+03;
ive 0; Mismatches 1;
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Fax: (206) 616-3887
Email: Jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2257 row: F column: 2
Class: BAC ends
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Location/Qualifiers
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In Onpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.,

Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Bavid B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greq Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www.bio.llni.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 162.
                                                                                                                                                                                                        /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 181)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                          /organism="Homo sapiens"
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/clone="RPCI-11 Human Wale BAC Library"
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100.0%; Pred. No. 1.2e+03
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/organism="Homo sapiens"
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/sex="Male"
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/lab_host="DH10B"
                          High quality sequence stop: 617.
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Gaps

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University of Washington
Seattle, WA 98195, USA
Fel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
                                                                                                                                                Sequence Tagged Connector
Plate: CT 807 row: J co
Class: BAC ends
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/tissue_type="adenocarcinoma cell line"
/tab_nost_="bH108 (phage-resistant).
/note="Organ: colon; Vector: powPg7; Site_]: XhoI; Site_2:
RcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size_selected >500bp for average insert size 1.8Kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
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1 (bases 1 to 359)

Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.F.

Construction of a Characterized Clone Resource for Genomic Sequencing; Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors

Unpublished (1997)

Contact: Mahairas GG, Zackrone KD, Hood L
      602455204F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583473 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"/db_xref="taxon:9606"
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                                                                                       BG386035.1 GI:13279481
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                                  mRNA sequence.
BG386035
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EST06143 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBB29 5° end similar to EST containing Alu Iepeat, mkNA sequence. T08352 T08252.1 GI:389280
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Adams, M.D., Soaces, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.
Rapid cDNA sequencing (expressed sequence tags) from a
directionally cloned human infant brain cDNA library
Nature Genet. 4, 373-380 (1993)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    /organism="Homo sapiens"
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/clone="Plate=CT 807 Col=11 Row=J"
/clone=lib="CIT Human Genomic Sperm Library C"
/sex="M"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108"
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Pred. No. 2.1e+03;
0; Mismatches 1; Indels 0
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94.4%; Pred. No. 2.1e+03;
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| RI c 110 g 90 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .382
/organism="Homo sapiens"
/db_xref="ATCC (inhost):84798"
/db_xref="taxon:9606"
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row: J column: 11
                                           High quality sequence stop: 359.
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us-09-904-420a-9.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 42)
Mahairas, G. G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E. Sequencing: Generation of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 444)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Hennott C.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chilko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
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/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"
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193604 MARC 2BOV Bos taurus CDNA 5', mRNA sequence.
BE723699
                                                                                                                                                                                                                                                                                    Hood L
                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Mahairas GG, Zackrone KD,
University of Washington
Seattle, WA 98195, USA
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/db_xref="taxon:9606"
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Location/Qualifiers
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Plate: CT 791 row: J co
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Fax: (206) 685-7301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&12-RC3-UT0062-210
800-011-e01&13-2000-08-21&t4-1)
Seq primer: pur 18 forward
High quality sequence start: 14
High quality sequence stop: 399.
                                                                                                                                                                                                                                                                                                                                         Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, C.S., Simpson, D.H., Brunstein, A., de Gollveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //note="Organ: uterus_tumor: Vector: puc18; Site_1: SmaI; Ste_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under 10w stringency conditions.
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                                                                                                              BE940403 399 bp mRNA EST 02-OCT-2000 RC3-UT0062-210800-011-e01 UT0062 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \operatorname{Simpson}, A.J. Shotgun sequencing of the human transcriptome with ORF expressed Shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 2.1e+03;
); Mismatches 1; Indels 0;
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                                                                                                                                                         BE940403
BE940403.1 GI:10469865
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94.48;
158 CCGAGGTGGGTCAT 175
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Gaps

us-09-904-420a-9.rst

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July of BAC End Sequences for Sequence-Ready Map Building
Obtober GSSs: RPCIII-11C13.TV
Other GSSs: RPCIII-11C13.TV
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: madadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
Research Genetics (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (htfo:/facegen.com). BAC end scarch/pac_end_search/bac_end_search/html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
4 (bases 1 to 470)
7 (bases 1 to 470)
8 (bases 1 to 470)
9 (bases

        B73071
        470 bp
        DNA
        GSS
        08-APR-1999

        RPCI11-11C13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11C13, DNA sequence.
        B73071
        GI:2712222

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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
98 c 102 g 112 t
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library" 119 c 86 g 140 t
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Pred. No. 2.1e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                          Score 16.4; DB 13;
Pred. No. 2.1e+03;
0; Mismatches 1;
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/db_xref="GDB:7503900"
/db_xref="taxon:9606"
/clone="RRCI-11-11013"
/clone_lib="RRCI-11"
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Matches 17; Conservative
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Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E. (Dases 1 to 455)
S. Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
L. Onbact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
             v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
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Clones are derived from the human BAC library RPC1-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieteredejong.med.buffalo.edu). Clones may be purchased from
BACBAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: SP6
Class: BAC ends.
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RPCIII-24H22.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24H22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref=""hARC 2BOV"
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/tissue_type="pooled"
/lab_host="PHIOB"
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/incte="Vector: pcnv sport6; Site_1: Xbal; Site_2: Xhol; Sit
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/sex="Male"
/cell_type="Lymphocytes"
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BACKWARD: GTTTCCCAGTACAGGACG
Plate: 38 row: I column: 18
Seq primer: ATTTAGGGTGACACTATAG.
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
BACPAC Resources (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institute on Deafness and Other Communication Disorders,
National Institutes of Health
5 Research Countr, Room 2A-15, Rockville, MD 20850, USA
Tel: 301 402 7580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .4', "
| .4', "Homo sapiens" | /organism="Homo sapiens" | /ob_xref="GUB:7540878" | /db_xref="taxon:9606" | /db_xref="taxon:9606" | /clone="RPCI-11-10747" | /clone="RPCI-11-10747" | /cel="type="Lymphocytes" | /cel="type="Lymphocytes" | /cel="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library" | /cel="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; /cote="Vector: pBACe3.6; Site_1: EcoRI; /cote="Vector: pBACe3.6; Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 471;
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Plate: 09 row: h column: 05
Seg primer: -28Ml3 reverse primer (Amersham)
Class: random plasmid subclone.
                                                                                               MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.1%; Score 16.4; DB 13;
94.4%; Pred. No. 2.1e+03;
Live 0; Mismatches 1;
                                                                                     9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="taxon:9606"
/clone="ew09h05"
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AZ757574.1 GI:13177040
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 471)
Adans.M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a random human BAC End Sequence Database for Sequence-Ready Map Building Unpublished (1998)
Other_GSSs: CIT-HSP-2385B22.TR.1
Other_GSSs: CIT-HSP-2385B22.TR.1
Department of Eukaryotic Genomics
The Institute for Genomic Research
772 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end Search page:
thtp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RPC111-107H7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-107H7,
                                                                            AQ240635 471 bp DNA GSS 30-SEP-1998
CIT-HSP-2385B22.TF.1 CIT-HSP Homo sapiens genomic clone 2385B22,
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/note="Vector: pBeloBAC11; Site_1: Hind111; Site_2:
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Pred. No. 2.1e+03;
0; Mismatches 1;
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/clone="2385B22"
/clone_lib="CIT-HSP"
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AQ240635.1 GI:3672833
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94.4%;
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Venter, J.C.
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AUTHORS
               RESULT 12
AQ240635
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Gaps

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 508) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                       /note="Vector: pGEM-T Easy; Human genomic DNA was partially digested with SauJAI, ligated to ds linkers, and enriched for blading to human PAX3/FKHR protein using a Whole Genome PCR-based strategy. DNA fragments containing putative PAX3/FKHR binding sites were amplified by PCR and cloned into pGEM-T Easy (Promega). The ligation products were transformed into DHIOB electrocompetent cells (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4; DB 13; Length 492; pred. No. 2.1e+03; 0; Mismatches 1; Indels 0
/clone_lib="PAX3/FKHR CASTing Library 'ew'"
/sex="Male"
/lab_host="DH10B"
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Location/Qualifiers
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GSS.
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Best Local Similarity 94.4%;
Matches 17; Conservative
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SUMMARIES

Homo sapiens
Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1115)
Mayer.K., Wolffe, E., Clevers, H. and Ballhausen, W.G.
The human high mobility group (HMG)-box transcription factor TCF-1:
novel isoforms due to alternative splicing and usage of a new exon 247361 H.sapiens T 247362 H.sapiens T X559809 Human TCF-1 X53901 Homo sapien X59871 Human TCF-1 AC009012 Homo sapi AC001336 Homo sapi AC01336 Homo sapi AC022298 Homo sapi AC022298 Homo sapi AC022298 Homo sapi AC01986 Homo sapi AC091986 Homo sapi AC09345 Homo sapi AC09345 Homo sapi AC093721 Homo sapi AC09374 Homo sapi AC09374 Homo sapi AC091364 Homo sapi AC091364 Homo sapi AC091364 Homo sapi AC073548 Homo sapi AC073548 Homo sapi AC073548 Homo sapi AC073648 Homo sapi AC073848 Homo sapi AC073848 Homo sapi AC073848 Homo sapi AC073848 Homo sapi AC07650 Drosophil Homo sapi Homo sapi Homo sapi Mus muscu Homo sapi Mus muscu Homo sapi Drosophil Homo sapi Sapi Drosophi HSTCFID 1115 bp mRNA PRI 09-JAN-1995 H.sapiens TCF-I mRNA for T cell factor 1 splice form D. 247361. 247361.1 GI:619881 splice form D; T cell factor 1. HOMO S HOMO Homo Unpublished

'groups' to 1115)

'groups' to 1115)

van de Wetering,M., Oosterwegel,M., Holstege,F., Dooyes,D.,
suijkerbuijk,R., Geurts van Kessel,A. and Clevers,H. Description AL359384 A AC079883 F AC079883 F AC07989 F AC025293 F AC0252732 F AC026478 AC060773 F AC060773 F AE503702 I AE503702 I AC010059 I AC07059 F AC010059 I AC07059 F AC010059 I AC07059 I AC07059 I AC07059 I AC07059 I AC07059 III AC07059 II ALIGNMENTS HSTCF1D HSTCF1E HSTCF1A HSTCF1B HSTCF1C AC009012 AC01336 AC01336 AC080017 AC08008 AC022298 AC069075 AC090345 AP003721 AC092736 AC024960 AC073548 AB046035 AC013963 AC013963 AC013963 AC013963 AC013963 AC079883 AC007650 AC069293 AC018890 AC018890 AC011108 AC090432 AC060773 AC004126 AC087673 AL590727 AC010059 AC018703 AP001986 100.0 1115
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Mayer,K., Wolff,E., Clevers,H. and Ballhausen,W.G.
The human high mobility group (HMG)-box transcription factor TCF-1: novel isoforms due to alternative splicing and usage of a new exon
                                                                                                                                                                                                                                                                                                                                                                                              /function="high mobility group box transcription factor"
                                                                                   % (bases 1 to 1115)
Ballhausen, W.G.
Ballhausen, W.G.
Bulission
Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
Location/Qualifiers
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H.Sapiens TCF-1 mRNA for T cell factor 1 splice form E.
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2 (bases 1 to 1165)
van de Wetering,M., Oosterwegel,M., Holstege,F., Dooyes,D.
rne human T cell transcription factor-1 gene. Structure, localization, and promoter characterization J. Biol. Chem. 267 (12), 8530-8536 (1992)
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splice form E; T cell factor 1.
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LPGEGRCPSCYPROSALGCPGSPARODSPSYHILLPREPTFILLTSTAERHHPQVSPL
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1 (bases 1 to 1254)
van de Wetering, M.
Direct Submission
Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,
                                                                                                                           Parallausen, W.G.
Ballhausen, W.G.
Brilhausen, W.G.
Direct Submission
Submitted (06.3AN-1995) Ballhausen W.G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
1. 1165
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DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene
Suijkerbuijk,R., Geurts van Kessel,A. and Clevers,H.
The human T cell transcription factor-1 gene. Structure,
localization, and promoter characterization
J. Blol. Chem. 267 (12), 8330-8536 (1992)
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25;
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Pred. No. 2
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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Futeleostomi;
Fukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2855)
Van de Wetering, M., Oosterwegel, M., Holstege, F., Dooyes, D.,
Suijkerbuijk, Geurts van Kessel, A. and Clevers, H.
The human T cell transcription factor-1 gene. Structure,
1 localization, and promoter characterization
3. Biol. Chem. 267 (12), 8530-8536 (1992)
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Van de Wetering, M., Castrop, J., Korinek, V. and Clevers, H.
Extensive alternative splicing and dual promotor usage generate
TCf-1 protein isoforms with differential transcription control
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96182076
3 (bases I to 2855)
Van de Wetering, M.L.
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EMBO J. 10 (1), 123-132 (1991)
91114695
See also X59869-X59871.
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1. .2814
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Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,
The Netherlands
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who de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H. Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1991
                      The Netherlands 2. (bases 1 to 1254)
2. (bases 1 to 1254)
van de Watering, M., Oosterwegel, M., Dooijes, D. and Clevers, H.
Identification and cloning of TCF-1, a T lymphocyte-specific
transcription factor containing a sequence-specific HMG box
EMBO J. 10 (1), 123-132 (1991)
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DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 2814)
van de Wetering,M.
Direct Submission
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24;
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Human TCF-1 mRNA for T cell factor 1 (splice form
X59970 X55329
X59870.1 G1:36787
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100.0%; Pred. No. 24;
ive 0; Mismatches
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Location/Qualifiers
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FMLYMKEMRAKVIAGTLKESARA INOILGRAWHALGREGORKYTELARKEPTHMOLLY
FMGNARDNYGKKKRRSREKHOESTTDPGSPKKCRARFGLNOOTDWCGPCR"
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht, The Netherlands
2 (bases 1 to 2910)
van de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H. Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box BMBO 1 10 (1), 123-132 (1991)
                                                                                                                                                                                   HSTCFIC 2910 bp mRNA PRI 17-JUN-1991
Human TCF-1 mRNA for T cell factor 1 (splice form C).
X59871, GI:36789
                                                                                                                                                                                                                                                                                                                             DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
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Location/Qualifiers
1. .2910
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T lymphocyte"
/cell_line="Jurkat and HPB-ALL"
/cloie_lib="conA"
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/note="atternative splice
860 c 671 g 597
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/evidence=experimental.
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/gene="TCF-1"
              872 ATTACCCACCCCCTCGGGA 891
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Direct Submission
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1811. 1799,1843. 1890,2054. 2134)
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Direct Submission
Submitted (07-JAN-1992) M.L. Van De Wetering, Department of
Immunology, P.O. Box 8550, 3508 GA Utrecht, THE NETHERLANDS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                /cell_type="T-lymphocyte"
/clone="phi-TCF-[5,8,11]"
/map="5q31.1"
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    .2855
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/db_xref="taxon:9606"
    /chromosome="5"

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Location/Qualifiers
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DOE Joint Genome Institute.
Direct Submission
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                                                                                                                                                                                                1 ordered pieces.
AC011336
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                                                                                                                                                                                                                                                                                                                       Homo sapiens
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AC011336/c
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 78189 bases at least Q40
Consensus quality: 82001 bases at least Q30
Consists of Size: 83944; sum-of-contigs estimation
Quality coverage: 6.34 in Q20 bases; pulse field qel estimation
Quality coverage: 6.34 in Q20 bases; pulse field qel estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 2979: contig of 2979 bp in length
* 3980
* 34576: contig of 24586 bp in length
* 59263
* 59362: gap of unknown length
* 59363
* 59362: gap of unknown length
* 76011
* 76101 76101 gap of unknown length
* 76011
* 76110 gap of unknown length
* 76111
* 79613: contig of 3636 bp in length
* 76111
* 79613: contig of 3636 bp in length
* 76111
* 79613: contig of 3636 bp in length
* 79714
* 80650
* 80749: gap of unknown length
* 79714
* 80650
* 80749: gap of unknown length
* 79714
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* 80749: gap of unknown length
* 79714
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* 80749: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submitted (03-ANG-1999) Production Sequencing Facility, DOE Joint Submitted (03-ANG-1999) Production Sequence Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:7454202.
                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 5 clone Xxpl-360D11, WORKING DRAFT SEGUENCE, 7 ordered pieces.
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21740 c 22203 g 20376 t
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Center Project Name: 1189075, H71
Center clone name: XXpl-360D11
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/organism="Homo sapiens"
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Center Code: JGI
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                AC009012.3 GI:12830104
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Best Local Similarity 100.
Matches 20; Conservative
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            DEFINITION
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TITLE
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AC011336 B6914 bp DNA HTG 23-APR-2001
Homo sapiens chromosome 5 clone CTC-250113, WORKING DRAFT SEQUENCE,
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1 (bases 1 to 86914)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Summary Statistics

Consensus quality: 82614 bases at least 040

Consensus quality: 86502 bases at least 030

Consensus quality: 86382 bases at least 020

Estimated insert size: 89000; pulse field qel estimation

Bstimated insert size: 89914; sum-of-contigs estimation

Quality coverage: 6.56 in 020 bases; pulse field gel estimation

Quality coverage: 6.56 in 020 bases; sum-of-contigs estimation

* NOME: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
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* of the gaps between them are based on estimates that have
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1 86914: contig of 86914 bp in length.
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22135 c 22612 g 21422 t
                                                                                                                                     AC011336.4 GI:9256274
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN
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Center clone name: CIT-HSPC_250113
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/db_xref="taxon:9606"
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TITLE COMMENT

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HTG 20-APR-2001 DNA HTG 20-APR-2001 Apmo sapiens chromosome 5 clone CTB-113120, WORKING DRAFT SEQUENCE, ACCOGGOB
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(bases 1 to 200831)

DOE Joint Genome Institute.

Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:7708985.

-----Genome Center
Center: Joint Genome Institute
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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                                                           gap of unknown length
contig of 4298 bp in length
gap of unknown length
contig of 7004 bp in length
gap of unknown length
contig of 5438 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2506 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of unknown length contig of 16291 bp in length gap of unknown length contig of 15639 bp in length.
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gap of unknown length
contig of 16248 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                            unknown length
of 13116 bp in length
unknown length
of 15377 bp in length
                                                                                                                                                                                                                                   gap of unknown length
contig of 9325 bp in length
gap of unknown length
contig of 6611 bp in length
                length
bp in length
                                                                                                                                                                                                                  in length
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                                                                                                                                                                             gap of unknown length
contig of 8327 bp in 1
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39367 a 38414 c 39218 g 39915 t
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Mismatches
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/db_xref*"taxon:9606"
/chromosome="5"
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Center Project Name: 107808, H233
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gap of
                                          contig
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143781: 0
159420: 0
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40746:
45044:
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95465:
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110942:
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75638:
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Best Local Similarity 100.0
Matches 20; Conservative
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127391
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143782
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110943
111043
33297
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AC008608
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AUTHORS
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AUTHORS
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KEYWORDS
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Consensus quality: 150910 bases at least Q30
Consensus quality: 150910 bases at least Q30
Consensus quality: 150910 bases at least Q30
Consensus quality: 152756 bases at least Q30
Estimated insert size: 800000; pulse field gel estimation
Estimated insert size: 80000; pulse field gel estimation
Quality coverage: 8.41 in Q20 bases; pulse field gel estimation
Quality coverage: 4.29 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will.
* be preserved.
                                               AC009017 159420 bp DNA HTG 20-APR-2001
Homo sapiens chromosome 5 clone XXpl-929G6, WORKING DRAFT SEQUENCE,
26 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (03-AdG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:11178048
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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unknown length
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Sequencing of Human Chromosome 5
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                         Consensus quality: 174733 bases at least Q40
Consensus quality: 186633 bases at least Q30
Consensus quality: 186633 bases at least Q30
Consensus quality: 190547 bases at least Q20
Estimated insert size: 165000; pulse field gel estimation
Estimated insert size: 188031; sum-of-configs estimation
Quality coverage: 7.77 in Q20 bases; sum-of-configs estimation
(unlity coverage: 6.47 in Q20 bases; sum-of-configs estimation

* NOTE: This is a "working draft' sequence. It currently

* consists of 29 configs. The true order of the pieces

* arbitrary. Gaps between the configs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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Nouse mouse.

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 112209)

SS Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C., Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J., Buhay,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z., Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M., Fornandez,J., Liu,W., Liu,W., Loulseged,H., Lozado,R.J., Martin,R., Noar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R., Perez,L., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Martin,R., Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watliquton,S., Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Watliquton,S., Worley,K. and Gibbs,R. Scherer,S., Sodergren,E., Weinstock,G., Morley,K.C.

Direct Submission

AL Onpublished

Direct Submission

AL Submitted (29-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (01-FEB-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Pavlor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC022298 112209 bp DNA ROD 23-MAR-2001
Mus musculus BAC RP23-423C8 (Roswell Park Cancer Institute Mouse
BAC Library) complete sequence.
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Worley, K.C.
Direct Submission
Submitted (31-JAN-2001) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One college of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                          BAC library B"
t 2823 others
137208: gap of unknown length 200831: contig of 63623 bp in length.
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                                                                                                                                                                                             /organism="Homo sapiens"
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Matches 20; Conservative
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Worley, K.C.
Direct Submission
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   complement(16199. .16311)
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10849. 11098

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/ CONA: AV271264"
Submitted (23-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On Jan 31, 2001 this sequence version replaced gi:12408434.

Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                                                                                                                                    Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

Location/Qualifiers
                                                                                                                                                                                                                                   Sequence similarities were identified using Powerblast by Jinghui
                                                                                                                                                                                The repeat regions shown were identified using RepeatMasker by
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/function="Overlaps with adjacent clone AC074046"
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11y="L1_MM" 5793

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1 (bases 1 to 13628)
Evans, G.A., Athanasiou, M., Aguayo, P., Armstronq, D., Basit, M.,
Evans, G.A., Athanasiou, M., Aguayo, P., Armstronq, D., Basit, M.,
Ebettner, J., Bunneister, R., Card, P., deSailboal, F., Dunn, J.,
English, C., Ethridge, S., Garner, H., Goe, V., Gordon, M., Gotway, G.,
Grant, O., Hahner, L., Harris, J., Lewis, E., Loo, H., Loo, K.N.,
Major, T., McFarland, J., Newton, J., Osborne-Lawrence, S.,
Schageman, J., Schultz, R.A., Stimson, S., Syed, M., and Ward, T.
HTGS Submission
Unpublished
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.
AC004126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%; Score 17.4; DB 2; Length 214780; 94.7%; Pred. No. 1.2e+02; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                       41175: contig of 41075 bp in length
41175: gap of unknown length
80399: contig of 39764 bp in length
81039: gap of unknown length
108744: contig of 27705 bp in length
1088744: gap of unknown length
137713: contig of 28869 bp in length
137813: gap of unknown length
163329: contig of 25916 bp in length
163329: contig of 25016 bp in length
163095: contig of 26206 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190195: gap of unknown length
206294: contig of 16099 bp in length
206394: gap of unknown length
210799: contig of 4405 bp in length
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213614: contig of 2715 bp in length
213714: gap of unknown length
214780: contig of 1066 bp in length.
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/db_xref="taxon:10090"
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39755 c 39241 g
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I (bases 1 to 214780)

Metarot. Lewis.L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Buandc, C., Burkett, C., Charko, J., Chen, G., Chen, G., Cox, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Goartell, J. H., Gunaratne, P., Haller, G., Hernandez, J., Hoques, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, J., Kovar, C., Liu, J., Liu, W., Loulseqed, H., Lozado, R. J., Martin, R., Massey, E., McLeod, M. P., Mel, G., Moore, S., Morgan, M., Marish, S., Perzz, L., Relter, D., Say, J., Shen, H., Vasquez, L., Watinforn, S., Muilliamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Muzny, D. M., Scherer, S., Sodergren, E., Weinstock, G., Noren, Suhmission, Suhmission, Suhmission
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Submitted (18-MAY-2000) Human Genome Sequencing Center, Department Submitted (18-MAY-2000) Human Genome Sequencing Center, Department Gamolecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77039, USA
On Jan 4, 2001 this sequence version replaced gi:11878525.

Center: Baylor College of Medicine
Center: Ganome Center
Center: BAYlor College of Medicine
Center: BAYLOR College of Medicine
Center: BAYLOR College of Medicine
Center: Project Information
Center project name: MAGG
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Sequencing vector: M13: L08823-35476
Sequencing vector: M13: L08823-35476
Chemistry: Dye-terminator Big Dye: 51% of reads
Chemistry: Dye-terminator Big Dye: 51% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 215130 bases at least 0.40
Consensus quality: 219207 bases at least 0.40
Consensus quality: 221311 bases at least 0.40
Consensus quality: 2020 bases; sum-contigs estimation
Quality coverage: 0.10 0.20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC069075 214780 bp DNA HTG 07-JAN-2001
Mus musculus chromosome 5 clone RP23-354F6, WORKING DRAFT SEQUENCE,
10 unordered pieces.
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                 Length 112209;
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                 87.0%; Score 17.4; DB 10; 94.7%; Pred. No. 1.4e+02;
                                   /rpt_family="(CAAAAA)n"
36674. .36854
/rpt_family="(GAAA)n"
complement(36859. .37401)
/rpt_family="L1"
                                                                                                                                                                                                                                                             0; Mismatches
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Worley, K.C.
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Gaps

904 others

		repeat_region complement(3034. 30612) repeat_region /rpt_family="Alu" repeat_region /rpt_family="MIR" repeat_region 41000. 41307		repeat_region /rpt_family=mir /rpt_family=mir /rpt_family=mir repeat_region complement(47422. 47487) /rpt_family=mir repeat_region complement(48093. 48170)		repeat_region 5553156814 /rpt_family="Alu" repeat_region complement(5821258345) /rpt_family="MIR" repeat_region 6105061105	repeat_region 6137761582 /rpt_family="LTR1" /rpt_family="LTR1" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="THE1" /rpt_family="THE1" repeat_region complement(6631966491)		repeat_region 77045.7733 repeat_region 77045.7733. repeat_region 78103.7830.78094) /rpt_family="FHEI" repeat_region 78103.78301 repeat_region 78300.80557 repeat_region 78300.80557 repeat_region 78000.80557	
Ward,T. and Wilson,R. TITLE Direct Submission JOURNAL Submitted (06-FEB-1998) Genome Science & Technology Center, University of Texas Southwester Medical Center, 5323 Harry Hines	Schageman, J., Schultz, R.A., Stimson, S., Syed, M. and Ward, T. TITLE Direct Submission JOGRNAL Submitted (20-JUM-1998) Genome Science & Technology Center, University of Texas Southwestern Medical Center, 5323 Harry Hines	COMMENT On Jun 20, 1998 this sequence version replaced gi:2842778. IMPORTANT: This submission contains the entire insert of clone pbJ606g6. pbJ606g6 comes from a PAC library constructed at the Roswell Park Cancer Institute by the Pieter de Jong group. This clone has been finished according to strict quality criteria and	attempts have been made to resolve all base calling problems such as compressions and repetitive elements. The expected Phracy Phrap calculated errors/10kb is 0.44. In addition, attempts have been made to assure over 99% of consensus base calls consist of either	CHECKER OF THIS PACT CLONE COMESTAND CHEMISTRY ON ONE CHECKER OF THE CHOMOSOMAL LOCUS: This PAC CLONE COMES From the Chromosome 11p12.2 Best's disease region mapped between STS D11S461 and EST AHNAK. This region spans over 1.5 Mbp. MARKER CONFIRMATION: Sequence confirmed STSs; D11S461, SHGC-36412, WI-12296	FEATURES Location/Qualifiers Source 1.1.136328 Acres Homo sapiens"	repeat_region 3. 111 /rpt_family="Alu" repeat_region 4399. 4574 repeat_region 54775700	repeat_region /rpt_family="Alu" repeat_region 8866. 9147 repeat_region 10302. 10604 /rpt_family="Alu"	repeat_region 108271119 repeat_region complement(1220812498) /rpt_family="Alu" /rpt_family="Alu" repeat_region complement(1357813749) /rpt_family="MRES9" repeat_region complement(1364713737) /rpt_family="MRES9" repeat_region complement(1380513947)	/rpt_family- complement(1) /rpt_family- complement(1) /rpt_family- rpt_family- complement(1) /rpt_family-	repeat_region complement(16650. 16934) /rpt_family=Alu" repeat_region complement(1897619291) /rpt_family="Alu" repeat_region 19340. 19651 /rpt_family="Alu"

us-09-904-420a-8.rge

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Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu.X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

L. Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 7, 2001 this sequence version replaced gi:13940671.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://fp.genome.washington.edu/RW/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   were stree; intep://www.seq.wn.intl.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: - Project Information
Center project name: L12228
Center project name: L12228
Center clone name: 68_H20
Center clone name: 68_H20
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155910 bases at least Q40
Consensus quality: 15585 bases at least Q30
Consensus quality: 156926 bases at least Q20
Insert size: 17000; agarose fp
Insert size: 177691; sum-of-contigs
Quality coverage: 7.5 in Q20 bases; sum-of-contigs
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46153 61179: contig of 15027 bp in length
61180 61279: gap of 100 bp
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91007 112059: contig of 21053 bp in lenyth
112060 112159: gap of 100 bp
112160 135292: contig of 23133 bp in lenyth
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135393 156663: contig of 2171 bp in length
155664 15668: gap of 100 bp
156664 158991: contig of 2328 bp in length.
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5561: contig of 4056 bp in length
1; gap of 100 bp
8335: contig of 2674 bp in length
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/db_xref="taxon:9606"
/chromosome="11"
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E (bases 1 to 158991)

S Birren B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, B., Campopiano, A., Choepel, Y., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J. Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Headrod, A., Horton, E., Hulme, W., Illav, I., Johnson, R., Jones, C., Karatas, A., LaNcque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marthews, C., McCque, K., Lamazares, R., Landers, T., Meheeters, R., Meldrim, J., Meneus, L., Mihova, T., Maenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schuuer, S., Schupback, R., Seaman, S., Severy, P.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-68H20
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Pred. No. 2e+02;
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/rpt_family="MER42"
complement(110662. .110778)
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'y="MER25"
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108358, 100/
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85422. .85697
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108079. .108201
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84880. .85169
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Best Local Similarity 100.0
Matches 17; Conservative
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TITLE
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NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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                                                                                                                                                                                                         Center clone name: FP11-68H20
Center clone name: FP11-68H20
Sequencing vector: PCR products; 100% of reads
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990229
Consensus quality: 157217 bases at least 040
Consensus quality: 159786 bases at least 030
Consensus quality: 159537 bases at least 020
Insert size: 160045; sum-of-contigs
Quality coverage: 9.33x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
Jan 4, 2001 this sequence version replaced 91:8117601
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120803: contig of 13746 bp in length
0903: gap of 100 bp
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120904 135414: contig of 14511 bp in length
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                                                         Center: RIKEN Genomic Sciences Center(GSC)
                                                                                         Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
                                                                                                                                       Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                             Center project name: HumDraftll
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E. (bases 1 to 161245)

B. (bases 1 to 161245)

E. Liyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Homo sapiens 161,245 genomic DNA of 11g

L. Published only in DataBase (2000) In press

E. 2 (bases 1 to 161245)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seoy, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

L. Submitted (02-MAY-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC).

Land Chemical Research (RIKEN), Genomic Sciences Center (GSC).

Land Chemical Research (RIKEN), Genomic Sciences Center (GSC).

Land Lattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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           /clone="RP11-68H20"
/clone_llb="RPCI-11 Human Male BAC"
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Pred. No. 2e+02;
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39985 c 39117 g 40263 t
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/note="assembly_fragment"

135393. 156563

/note="assembly_fragment"

156664. 158991

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HTG; HTGS_PHASE1; HTGS_DRAFT.
HOmo sapiens DNA, clone:RP11-68H20.
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662. .8335
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clone_end:SP6
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SEQUENCE, 13 unordered pieces.
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Search completed: February 20, 2002, 11:02:39
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Human genomic DNA	E. praecox ssrRNA.	Eimeria praecox ss	E. mitis ssrRNA.	E. mitis ssrRNA.	Elmeria mitis ssrR	Eph-related PTK Ce	Roh-related PTK Ce	Human secreted oro	Trichoderma reesei	Human cervical can
SUMMARIES			ID		AA162833	AAQ31327	AAQ31643	AAQ31325	AAQ31472	AAQ31629	AAQ90660	AA090657	AAC 08 0 6 9	AAF14929	AAH70729
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31-JAN-2000; 2000US-0179065. 04-FEB-2000; 2000US-0180628. 19-MAY-2000; 2000US-0205515. 07-JUL-2000; 2000US-0216880. 14-JUL-2000; 2000US-0218290. 14-AUG-2000; 2000US-0229447. 01-SEP-2000; 2000US-0229343.

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o c	23			0	343		AAT51191	
ט	24		4	0	508		AAQ31287	gment 4, a
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ΧX	anti	parasi	tic; (cardi	ant;	imm	une disorder; cardiova	scular disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM42347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. crebral anoxia and cepilepsy; and (f) infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.0%; Score 17; DB 22; Length 26555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 161; 532pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26555 BP; 5916 A; 7244 C; 7332 G; 6063 T; 0 other;
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 06-SEP-2000; 2000US-0230437.
25-SEP-2000; 2000US-0231243.
25-SEP-2000; 2000US-0231243.
29-SEP-2000; 2000US-0239937.
13-CCT-2000; 2000US-0239937.
08-NOV-2000; 2000US-0239937.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246525.
08-NOV-2000; 2000US-0246526.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-024921.
17-NOV-2000; 2000US-024921.
17-NOV-2000; 2000US-02998.
17-NOV-2000; 2000US-0250391.
18-EC-2000; 2000US-0250391.
18-EC-2000; 2000US-0250391.
18-EC-2000; 2000US-0250391.
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Best Local Similarity 100.
Matches 17; Conservative
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NOTE: As specifications EP-516381, EP-516391 and EP-516395-6 are identical except in the claims section, sequences contained value and the sequences of each specification will be indexed under their own patent number, thus each separate patent will be indexed represented.
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                                                        Small subunit; ribosomal RNA; amplification; PCR; Eimeria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chakraborty PR, Dashkevicz M, Elbrecht A, Feighner SD;
Liberator P, P-Juchelka H;
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92US-0879469.
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Best Local Similarity 89.5
Matches 17; Conservative
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E. praecox ssrRNA.
                                                                                                                                                                                                                                                                                                                                 29-MAY-1991;
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                                                                                                                                                                                                                                                              27-MAY-1992;
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(MERI ) MERCK & CO INC.
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12-MAY-1992;
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of small subunit ribosomal RNA sequences with near identity in the
eukaryotic kingdom identified two consensus sequences. ERIB 1 and
ERIB 10. Taken together, these two oligonucleotides span the vast
c ERIB 10. Taken together, these two oligonucleotides span the vast
in PCR to selectively amplify the ssrRNA sequence may then be used
consistent of the srrRNA sequence. The ssrRNA sequence may then be used
to design species specific probes for diagnosis of Eimeria praecox
infection, e.g. regions 106-113, 153-179, 188-223, 253-266,
1514 and 1664-1699 (claimed) which are complemetary to the ssrRNA
gene of E. praecox. See also AAO31640.2
CNOTE: As specifications EP-516381, EP-516391 and
gene of E. praecos of seal so and the claims section, sequences
for all these specifications can be found indexed under EP-516385.
CHOWEVER the Inumber, thus each separate patent will be indexed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                         Species-specific Eimeria tenella DNA probes – comprise divergent
DNA sequences and are complementary to E. tenella small sub-unit
ribosomal RNA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.8; DB 13; Length 1747; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Small subunit; ribosomal RNA; amplification; PCR; Eimeria; ss.
                                                                                                         Elbrecht A, Feighner SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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ID AAQ31325 standard; DNA; 1749 BP.
                                                                                                        PR, Dashkevicz M,
P-Juchelka H;
                                                                                                                                                                                                  Claim 10; Fig 6; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1502 ATTACCCAGCCCCATCGGG 1484
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                                   92EP-0304780.
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                                                      91US-0707360.
92US-0879594.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.0
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                     (MERI ) MERCK & CO INC.
                                                                                                                                       WPI; 1992-400735/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. mitis ssrRNA.
                                                                                                         Chakraborty Pl
Liberator P,
                                   27-MAY-1992;
                                                      29-MAY-1991;
12-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-1991;
12-MAY-1992;
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               02-DEC-1992.
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Comparative analysis of regions close to both the 3' and 5' ends core small subunit ribosomal RNA sequences with near identity in the elekaryotic kingdom identified two consensus sequences. BRIB 1 and ERIB 10. ERIB 1 represents a consensus sequence less than 10 conclections from the 3' end of eukaryotic ssrRNA genes. The ERIB 10 conclections from the 3' end of eukaryotic ssrRNA genes. Taken together, these two oligonucleotides span the vast majority of Taken together, these two oligonucleotides span the vast majority of the ssrRNA genes sequence, and they were used as a primer pair in PCC amount of the ssrRNA genes of the ssrRNA sequence of proper in the strRNA sequence of proper in the strRNA sequence of Einerla mitis infection. See also AAQ11283-332.

Conference of the strBNA sequences of the strBNA sequence of the strBNA sequence of the strBNA sequence of Einerla mitis infection. See also AAQ11283-332.

Conference of the strBNA sequence of the specifications section, sequences of for all these specifications can be found indexed under EP-516385.

Characterial their own patent number, thus each separate patent will be indexed the sequences.
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                                                                                                                                                                            Species-specific Eimeria tenella DNA probes – comprise divergent DNA sequences and are complementary to E. tenella small sub-unit ribosomal RNA gene
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Feighner SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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89.5%; Pred. No. 1.6e+02;
       Elbrecht A,
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                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 4; 79pp; English.
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Liberator P, P-Juchelka H;
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       Chakraborty PR, Dashkevicz
Liberator P, P-Juchelka H;
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920S-0879585.
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Best Local Similarity 89.5
Matches 17; Conservative
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Query Match
Best Local Simi
Matches 17; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proquosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus sp.
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                                                                    Comparative analysis of regions close to both the 3' and 5' ends of small subunit ribosomal RNA sequences with near identity in the cukaryotic kingdom identified two consensus sequences. FRIB 1 and ERIB 10. ERIB 1 represents a consensus sequence loss than 10 nucleotides from the 5' end of eukaryotic ssrRNA genes. The ERIB 10 sequence is the inverse complement to a consensus sequence located approx. 20 nucleotides from the 3' end of eukaryotic ssrRNA genes. Taken together, these two oligonucleotides span the vast majority of the ssrRNA gene sequence, and they were used as a primer pair in PCR to selectively amplify the ssrRNA genes contained within the genomic DNA prepd. from Eimeria mitis. The ssrRNA sequence may then be used to design a species specific probes for diagnosis of Eimeria mitis infection (method claimed). See also AAQ31465-71.

NOTE: As specifications EP-516381, EP-516383-6, EP-516391 and EP-516395-6 are identical except in the claims section, sequences of for all these specifications can be found indexed under EP-516386. Conder the claimed sequences of each specification will be indexed to constitute their own patent number, thus each separate patent will be
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Species-specific Eimeria tenella DNA probes - comprise divergent DNA sequences and are complementary to E. tenella small sub-unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species-specific Eimeria tenella DNA probes – comprise divergent DNA sequences and are complementary to E. tenella small sub-unit ribosomal RNA gene
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                                                                                                                                                                                                                                                                                                                     Sequence 1749 BP; 437 A; 362 C; 465 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Small subunit; ribosomal RNA; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                         Score 15.8; DB 13;
Pred. No. 1.6e+02;
0; Mismatches 2;
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                                                Disclosure; Fig 4; 79pp; English.
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1 Similarity 89.5%;
17; Conservative (
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92US-0879640.
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Liberator P, P-Juchelka H;
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                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
Matches 17; Conserv
                          ribosomal RNA gene
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cukaryotic kingdom identified two consensus sequences, ERIB 1 and eukaryotic kingdom identified two oingonuclectides span the vast ERIB 10. Taken together, these two oingonuclectides span the vast in PCR to selectively amplify the ssrRNA gene contained within genomic DNA prepd. from Eimeria mitis. The ssrRNA sequence may then be used to design species specific probes for diagnosis of Eimeria mitis. Confection, e.g. regions 106-113, 153-179, 188-223, 253-266, 630-725, 933-928, 1026-1041, 1051-1057, 1149-1161, 1329-1380, 1474-1517 and 1667-170, (ctaimed) which are complemetary to the ssrRNA gene of E. mitis. See also AAQ31626-8.

NOTE: As specifications EP-516381, EP-516383-6, EP-516391 and EP-516395-6 are identical except in the claims section, sequences for all these specifications can be found indexed under EP-516385. However the claimed sequences of each specification will be indexed under their own patent number, thus each separate patent will be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probes derived from the EPH-related PTKs Cek4 (AAQ90659) and Cek5 (AAQ90660) were used to isolate novel cDNA clones (AAQ90652-58, AAQ90661-62) from chicken embryo and embryonic brain libraries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.0%; Score 15.8; DB 13;
89.5%; Pred. No. 1.6e+02;
Live 0; Mismatches 2;
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17; Conservative
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us-09-904-420a-8.rng

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyAr FRNAs derived from 30 different Lissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-d' primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer. CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore bused to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forenist, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                    Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum: Aspergillus niger; Aspergillus oryzae; Trichoderma reesci; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; sa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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Pred. No. 2.4e+02;
0; Mismatches 1;
                                                                            Human secreted protein 5' EST, SEQ ID NO: 12144.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 12144; 71pp + CD-ROM; English.
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Best Local Similarity 94.1%;
Matches 16; Conservative
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                                        06-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET.
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                              EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                        26-FEB-1999;
                                                                                                                                                                                                                                                                         06-SEP-2000.
AAC08069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF14929;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A cDNA clone encoding a novel variant of EPH-related PTK Cek5, Cek5+ (AAQ90657), was isolated from a chick embryo library in lambda gtll. Cek5+ protein (AAR75709) contains a 16-amino acid insertion in the juxtamembrane domain, and be a result of alternative splicing. Cek5+ is exclusively expressed in the CNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                     0;
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                                                            Length 4049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein tyrosine-kinase; PTK; cancer; diagnosis;
  Sequence 4049 BP; 1010 A; 1011 C; 1072 G; 956 T; 0 other;
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4097 BP; 1014 A; 1029 C; 1087 G; 967 T; 0 other;
                                                          Query Match 79.0%; Score 15.8; DB 16; Best Local Similarity 89.5%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 71-75; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
10..3045
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                                                                                                                                                                           AAQ90657 standard; DNA; 4097 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC08069 standard; cDNA; 483 BP
                                                                                                                                                                        3686 ATTCCCCACCCCCGGG 3668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3734 ATTCCCCACCCCCCGGG 3716
                                                                                                                                               1 attacccaccccctcggg 19
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                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Eph-related PTK Cek5+.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-215256/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prognosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eph;
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Gallus sp.

Key

Cek5+;

AAQ90657;

AA090657/c

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Gaps

0;

Length 483; Indels

cancer

AAC08069/c ID AAC080 XX

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the Fr cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway englas one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate and malysis of the results. AAF07478 to AAF11877 represents ESTS from Aspergillus nights in the condition of the gene products to facilitate analysis of the results. BAF078 from Aspergillus oryzae; and AAF11879 to AAF11873 represents ESTS from Aspergillus oryzae; and CAAF11877 represents ESTS from Aspergillus oryzae; and CAAF11879 to AAF11877 represents ESTS from Aspergillus oryzae; and CAAF11879 to AAF11877 represents ESTS from Aspergillus oryzae; and CAAF11870 to AAF11870 from Aspergillus represents ESTS from Aspergillus oryzae; and CAAF11870 from AAF11870 from Aspergillus represents ESTS from Aspergillus and ESTS from AAF11870 from AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
O
                                                                                                                                                                                                                                                                                                                                                                                                              Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags \cdot
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                                                                                                                                                                                                                                                                                                                            Olsen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 2.4e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                            Clausen IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 875 BP; 186 A; 239 C; 215 G; 207 T; 28 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cervical cancer marker nucleic acid 2003.
                                                                                                                                                                                                                                                                                                                            Shuster JR, Kauppinen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 89; Page 3009; 3161pp; English
                                                                                                                                                                                                                                                         (NOVO ) NOVO NORDISK BIOTECH INC (NOVO ) NOVO NORDISK AS.
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88.9%;
                                                                                                                                                                  22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                                            99US-0273623
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                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-594572/56.
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les 16; Conserv
                                                                                                                                                                                                                                                                                                                                 Rey MW,
                                Trichoderma reesei.
                                                                          WO200056762-A2.
                                                                                                                                                                                                              22-MAR-1999;
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                                                                                                                       38-SEP-2000
                                                                                                                                                                                                                                                                                                                                 Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH70729:
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Matches
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cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition: to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated nucleic acid for diagnosing and treating cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for assessing and detecting compounds for treating the cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein encoding cDNA (clone Id HBOEG11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 902 BP; 236 A; 200 C; 221 G; 242 T; 3 other;
                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                      Berger A, Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 427; 1051pp; English.
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                                                                                                                                               99US-0169681.
99US-0171350.
2000US-0189315.
2000US-0203791.
2000US-0210600.
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2000US-0180628.
2000US-0231968.
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                                                                                               2000WO-US33312.
                                                                                                                                                                                                                                                                                   2000US-0220114.
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                                                                                                                                                                                                                                                                                                                                                                                        Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200155430-A1.
WO200142467-A2.
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04-FEB-2000;
12-SEP-2000;
                                                                                                                                                                                                    14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                  08-DEC-2000;
                                                                                                                                                                                                                                                                                   21-JUL-2000;
                                                                                                                                                  08-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                      Schlegel R,
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                                             14-JUN-2001
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P-PSDB; AAB88395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme closed include autoimmune diseases e.g. radioimmunoassays or enzyme treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypetides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present
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                                      Birse CE, Soppet DR, Olsen HS;
Shi Y, Choi GH, Fiscella M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                17\, isolated nucleic acid molecules encoding human secreted proteins, used to preventing, treating or ameliorating a medical condition -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA encoding a membrane or secretory protein clone PSEC0143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4; DB 22; Length 1867;
Pred. No. 2.4e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1867 BP; 542 A; 315 C; 347 G; 663 T; 0 other;
                                                                                                                                                                        Claim 1; Page 414-415; 482pp; English.
                                      Baker KP,
Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF93822/c
ID AAF93822 standard; cDNA; 1976 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.0%;
ilarity 94.1%;
Conservative (
           (HUMA-) HUMAN GENOME SCI INC.
                                     CA, Komatsoulis GA, E
PA, Wei P, Ebner R,
Ruben SM, Barash SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1999; 99JP-0194179.
11-JAN-2000; 2000JP-0118775.
02-MAY-2000; 2000JP-0183766.
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                                                                                          WPI; 2001-476220/51.
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Best Local Similarity
Matches 16; Conserv
                                                                                                       P-PSDB; AAB85525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-2001
                                        Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF93822;
                                                   Moore PA,
                                                                  Ni J,
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This invention relates to nucleic acid sequences AAF93744 - AAF93916
which encode human secretory or membrane proteins represented by
AAB8817 - AAB8849. Included in the invention are primers
AAB8817 - AAB8849. Included in the invention are primers
CAAB8817 - AAB8849. Included in the invention are primers
CC AAB8817 - AAF92255 and AAF62235 which are used to isolate the
Production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC an be used in gene therapy. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences
CC proteins they encode may be used with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic asso be
CC sequences and also be used as DNA probes in diagnostic asso be
CC used to similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC antify modulators (agonists and antabolism. The polypeptides may be used
CC activity. The antibodies and antaponists may also be used as diagnostic agents for detecting the presence of the
CC be used as diagnostic agents for detecting the presence of the
CC be used as diagnostic agent which may be treated include rheumatoid
CC arthirities and diseases which may be treated include rheumatoid
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                                                                                                                                                                                                                                                                               Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                   Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1976 BP; 595 A; 314 C; 371 G; 696 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.4; DB 22;
Pred. No. 2.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID 157; 609pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA sequence SEQ ID NO:11070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH13994 standard; cDNA; 2311 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 attacccaccccctcg 17
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(HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arthritis and diabetes.
                                                                                                                                                                 WPI; 2001-093989/11.
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us-09-904-420a-8.rng

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 3'-end sequence, where the oligonucleotide comprises a 3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the contection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the cDNAs easily without any specialised methods. AAH318528 and AAH38583 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; human;
                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                 Saito K, Yamamoto J;
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.4; DB 22; Length 2311;
Pred. No. 2.4e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein encoding cDNA (clone Id HBOEG11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2311 BP; 655 A; 382 C; 458 G; 816 T; 0 other;
                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 11070; 2537pp + CD ROM; English.
                                                                                                    nikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opthalmalogical; gene therapy; ss.
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                                                                                                    Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH46951/c
ID AAH46951 standard; cDNA; 3076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.18;
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 attacccaccccctcg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the present invention
                                                            (HELI-) HELIX RES INST.
                                                                                                                          Sugiyama T,
                                                                                                                                                              WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                      Isogai T,
                                                                                                                                                                                                                                                                    full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001
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                                                                                                                        Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
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Search completed: February 20, 2002, 10:32:01

Job time: 10229 sec

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The invention provides novel human secreted proteins and polynucleotides concoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnosit immunosassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, or phyperpides and also be coular disorders e.g. corneal infection. The polyperides can also be coular disorders e.g. corneal infection. The polyperides can also be supporting cell culture of primary tissues, to reqenetate tissues and in chemotaxis. The polypeptides can also be used as a food additive or chemotaxis. The polypeptides can also be used as a food additive or concase in the present and provider conditions can be nown ascreted protein encoding cDNA.
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                                                                                                                                                                             Birse CE, Soppet DR, Olsen HS;
Shi Y, Choi GH, Fiscella M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                17 isolated nucleic acid molecules encoding human secreted proteins, used to preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.0%; Score 15.4; DB 22; Length 3076; 94.1%; Pred. No. 2.4e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3076 BP; 940 A; 487 C; 617 G; 1028 T; 4 other;
                                                                                                                                                                                  Baker KP,
Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 426-427; 482pp; English.
                                          2000US-0179065.
2000US-0180628.
2000US-0231968.
                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                  Rosen CA, Komatsoulis GA,
Moore PA, Wei P, Ebner R,
Ni J, Ruben SM, Barash SC;
17-JAN-2001; 2001WO-US01431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                              WPI; 2001-476220/51.
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Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                          P-PSDB; AAB85541
                                               31-JAN-2000;
                                                                                            12-SEP-2000;
                                                                        04-FEB-2000;
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us-09-904-420a-8.rni

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TELEX: 138825
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
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                     0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Sequence 29, Sequence 29, Sequence 29, Sequence 29, Sequence 29, Sequence 27, Seque
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/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-879-647A-29

US-07-879-584A-29

US-07-879-640A-29

US-07-879-640A-29

US-07-879-640A-29

US-07-879-640A-29

US-07-879-64A-27

US-07-879-64A-27

US-07-879-64A-27

US-07-879-64A-27

US-07-879-64A-27

US-08-162-809-11

PCT-US-08-162-809-13

US-08-162-809-13

US-08-162-809-13

US-08-162-809-13

US-08-162-809-13

US-07-879-64A-50

US-07-879-64A-25

US-07-879-544A-25

US-07-879-584A-25
                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
                                                                                                                                                                                                                               351203 seqs, 113238999 residues
                                                                                          February 20, 2002, 07:44:49;
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                                                                                                                                                                                                                                                                                                                     Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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                                                                                                                                                                     attacccaccccctcggga
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                                                                                                                                       US-09-904-420A-8
20
                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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Perfect score:
                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number
                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                                     OM nucleic
                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                   Searched:
                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
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224,
224,
226,
226,
226,
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Sequence
Sequence
  sed neuce sed ne
US-07-879-644A-25
US-07-879-640A-25
US-07-879-594A-25
US-07-879-647A-24
US-07-879-584A-24
US-07-879-584A-24
US-07-879-594A-24
US-07-879-594A-24
US-07-879-594A-24
US-07-879-594A-26
US-07-879-594A-26
US-07-879-544A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Elbrecht, A.
APPLICANT: Feighner, S.D.
APPLICANT: Feighner, S.D.
APPLICANT: Liberator, P.A.
TITLE OF INVENTION: Eimeria Maxima DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette,3.50 inch,800 MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 6.0.4 SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/879,647A FILING DATE: 19920512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 415
PRIOR APPLICATION DATA:
APPLICATON UNMBER: 07/706,628
FILLIG DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-07-879-647A-29/c
; Sequec 29, Application US/07879647A
patent No. 5266689
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Merck & Co., Inc.
126 Lincoln Avenue
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chakraborty, P.R. APPLICANT: Dashkevicz, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (908) 594-53:
(908) 594-4720
                            COMPUTER READABLE FORM:
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                    APPLICANT: Chakraborty, P.R.
APPLICANT: Chakraborty, P.R.
APPLICANT: Elbrecht, A.
APPLICANT: Felighner, S.D.
APPLICANT: Felighner, S.D.
APPLICANT: Liberator, P.A.
APPLICANT: Liberator, P.A.
APPLICANT: Drofous Juchelka, H.
TITLE OF INVENTION: Eimeria Necatrix DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eimeria Acervulina DNA
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MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE DOCKET NUMBER: 18422IA
TELECOMMUNICATION INFORMATION:
TELEFAX: (908) 594-5321
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 bases
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 6.0.4 SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA: 19920512 FILING DATE: 19920512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19920512
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,351
FILING DATE: 29-MAY-1991
ATTONEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/07879644A; Patent No. 5298613; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chakraborty, P.R. APPLICANT: Dashkevicz, M. APPLICANT: Elbrecht, A. APPLICANT: Felghner, S.D. APPLICANT: Liberator, P.A. APPLICANT: Profous-Juchelka, H. APPLICANT: Profous-Juchelka, H.
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ADDRESSEE: Merck & Co., Inc.
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Best Local Similarity 89.5%
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  SIRELL.
CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
    GENERAL INFORMATION:
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US-07-879-644A-29/C
                                                                                                                                                                                                                                                                                                                                             07065
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US-07-879-470A-29
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                                                 Gaps
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      Length 1747;
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                                                 Indels
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    79.0%; Score 15.8; DB 1;
89.5%; Pred. No. 43;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%; Score 15.8; D
89.5%; Pred. No. 43;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Elbrecht, A. A. APPLICANT: Feighner, S.D. APPLICANT: Feighner, S.D. APPLICANT: Liberator, P.A. APPLICANT: Profous Juchelka, H. TITLE OF INVENTION: Eimeria Brunetti DNA TITLE OF INVENTION: probes NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/879,584A FILING DATE: 19920512 CLASS/FICATION DATA: PRIOR APPLICATION NUMBER: 07/706,717 APPLICATION NUMBER: 07/706,717 FILING DATE: 29-MAY-1991 ATTORNEY/AGENT INFORMATION: NAME: TAIBBLE, Jack L. REFERENCE/DOCKET NUMBER: 32,633 REFERENCE/DOCKET NUMBER: 184191A TELECHOME: (908) 594-5321 FIELERHONE: (908) 594-5321 FIELERHONE: (908) 594-5321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                              RESULT 2
US-07-879-584A-29/C
IS-07-879-584A-29/C
Squence 29, Application US/07879584A
Patent No. 5278298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
                                                                                                                 Db 1502 ATTACCCAGCCCATCGGG 1484
                                                                                                                                                                                                                                                                                                  Chakraborty, P.R.
Dashkevicz, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1502 ATTACCCAGCCCCATCGGG 1484
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INFORMATION FOR SEQ ID NO: 29
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 bases
TYPE: NUCLEIC ACID
                                                                                        1 attacccaccccctcggg 19
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Query Match
Best Local Similarity 89.59
Matches 17; Conservative
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Best Local Similarity 89.5'
Matches 17; Conservative
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APPLICANT: Chakral
APPLICANT: Dashke
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US-07-879-470A-29/C
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MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
MEDIUM TYPE: Storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,594A
FILING DATE: 19920512
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 79.0%; Score 15.8; D Best Local Similarity 89.5%; Pred. No. 43; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Elbrecht, A.
APPLICANT: Feighner, S.D.
APPLICANT: Liberator, P.A.
APPLICANT: Liberator, P.A.
APPLICANT: Profous-Juchelka, H.
TITLE OF INVENTION: Eimeria Praecox DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
                    CLASSIECCATION: 536
PRIOR APPLICATION DATA
APPLICATION NUMBER: 07/706,355
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
RECISTRATION NUMBER: 32,633
RECISTRATION NUMBER: 32,633
TELEPHONE: (908) 594-521
TELEPHONE: (908) 594-521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184231A
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APPLICATION DATA:
APPLICATION NUMBER: 07/706,360
FTILING DATE: 29-MAY-1991
ATTORNEY/ACENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 33,633
REFERENCE/DOCKET NUMBER: .184231A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
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TELECOMMUNICATION:
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; Sequence 29, Application US/07879594A
; Patent No. 544976
; GENERAL INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chakraborty, P.R. APPLICANT: Dashkevicz, M.
                                                                                                                                                                                                                                                                                                               TELEFACT...
TELEFACT. 138825
TELEX. 138825
INFORMATION FOR SEQ ID NO: 2'S SCUIENCE CHARACTERISTICS:
LENGTH: 1747 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
19920512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 12b DENESTED TO STREET: 12b DENESTED STATE: New Jersey
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ZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-07-879-640A-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
MEDIUM TYPE: storage
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
MEDIUM TYPE: storage
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APPLICANT: Dashkevicz, M.
APPLICANT: Elbrecht, A.
APPLICANT: Feighner, S.D.
APPLICANT: Liberator, P.A.
APPLICANT: Liberator, P.A.
TITLE OF INVENTION: Eimeria Mitis DNA
TITLE OF INVENTION: Probes
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OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,640A
                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,644A
FILING DATE: 19920512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .18418IA
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/706,817
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: .18418L/
TELECOMMUNICATION INFORMATION:
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Sequence 29, Application US/07879640A
Patent No. 5359050
GENERAL INFORMATION:
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126 Lincoln Avenue
                126 Lincoln Avenue
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(908) 594-4720
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TELEX: 138825
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Merck & C
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CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
      STREET: 126 Linco
CITY: Rahway
STATE: New Jersey
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US-07-879-644A-29
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89.5%; Pred. No. 43;
Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,3.50 inch,800 Kb
MEDIUM TYPE: Storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: M.Crosoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,647A
FILING DATE: 19990512
                                  RESULT 8
US-07-875/C
Sequence 27, Application US/07879647A
Sequence 27, Application US/07879647A
Patent No. 5286689
GEMERAL INFORMATION:
APPLICANT Chakraborty, P.R.
APPLICANT Elbrecht, A.
APPLICANT Elbrecht, A.
APPLICANT Elbrecht, P.A.
APPLICANT ESTENETH STORESS:
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
RIRETER.
STREFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19920512
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,628
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/07879584A
Patent No. 527829
GENERAL INFORMATION
APPLICANT: Chakraborty, P.R.
APPLICANT: Bashkevicz, M.
APPLICANT: Elbrecht, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1505 ATTACCCACGCCCATCGGG 1487
                   1502 ATTACCCAGCCCCATCGGG 1484
1 attacccaccccctcggg 19
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INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
Matches 17; Conserv
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US-07-879-647A-27
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                                                                                                                                                                                Query Match 79.0%; Score 15.8; DB 1; Length 1747; Best Local Similarity 89.5%; Pred. No. 43; Matches 17; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1747;
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MEDIUM TYPE: Diskette,3.50 inch,800 Kb
MEDIUM TYPE: storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,469A
FILING DATE: 19920512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%; Score 15.8; 89.5%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Elbrecht, A.
APPLICANT: Feighner, S.D.
APPLICANT: Liberator, P.A.
APPLICANT: Profous-Juchelka, H.
TITLE OF INVENTION: Eimeria Tenella DNA
TITLE OF INVENTION: Probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .18424IA
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/07879469A Patent No. 5563256 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19920512
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,362
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 1847
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-5720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
                                                                                                                                                                                                                                                                                       DD 1502 ATTACCCAGCCCCATGGG 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chakraborty, P.R.
Dashkevicz, M.
                                                                                                                                                                                                                                                                 1 attacccaccccctcggg 19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 138825
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rahway
STATE: New Jersey
COUNTRY: USA
                                                                                                        linear
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US-07-879-469A-29
                                                                                                      TOPOLOGY:
US-07-879-594A-29
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-07-879-644A-27/C
Sequence 27, Application US/07879644A
APPLICANT: Chakraborty, P.R.
APPLICANT: Elbercht, A.
APPLICANT: Fighner, S.D.
APPLICANT: Profous Juchelka, H.
TITLE OF INVENTION: Elmeria Acervulina DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck A.C.
STREFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,3.50 inch,800 Kb
MEDIUM TYPE: storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,3.50 inch,800 Kb
MEDIUM TYPE: storage
                                               MEDIUM TYPE: storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA
APPLICATION DATE: 1920512
CLASSIFICATION DATA
CLASSIFICATION DATA
APPLICATION UNBER: 07/706,351
FILING DATE: 19920512
APPLICATION UNBER: 07/706,351
FILING DATE: 19920512
APPLICATION NUBER: 32,633
REFERENCE/DOCKET NUMBER: 3,633
REFERENCE/DOCKET NUMBER: 3,633
REFERENCE/DOCKET NUMBER: 18421A
TELEPHONE: (908) 594-4720
TELEPHONE: (908) 594-5321
TELEPAX: (908) 594-5321
TELEPAX: (908) 594-5321
TELEPAX: 138625 IN NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1749 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,644A
FILING DATE: 19920512
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FILING DATE: 1992UDLE
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,817
...C DATE: 29-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 1505 ATTACCCAGGCCCATCGG 1487
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Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: single
; TOPOLOGY: linear
US-07-879-470A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 126 Lincoln CITY: Rahway STATE: New Jersey COUNTRY: USA ZIP: 07065
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Pest Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette,3.50 inch,800 Kb MEDIUM TYPE: DISKette,3.50 inch,800 Kb MEDIUM TYPE: DISKette,3.50 inch,800 Kb MEDIUM TYPE: Storage COMPUTER: Apple Macintosh 6.0.4 SOFTWARE: Apple Macintosh 6.0.4 SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA: PILING DATE: 19920512 CLASSIFICATION NUMBER: US/07/879,584A FILING DATE: 19920512 APPLICATION NUMBER: US/07/6,717 FILING DATE: 29 MAY-1991 APPLICATION NUMBER: 32,633 REPRENEE/DOCKET NUMBER: 184191A TELEPAN: (908) 594-5321 TELEPAN: (908) 594-5321 TELEPAN: 138825 INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS: LENGTH: 1749 bases LENGTH: 1749 bases TYPE NUCLEIC ACID STRANDENESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-879-470A-27/C
Sequence 27, Application US/07879470A
Patent No. 5288845
GENERAL INFORMATION:
APPLICANT: CHARTADOTTY, P.R.
APPLICANT: Bibrecht, A.
APPLICANT: Elbrecht, A.
APPLICANT: Liberator, P.A.
APPLICANT: Profous-Juchelka, H.
TITLE OF INVENTION: Eimeria Necatrix DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
           APPLICANT: Feighner, S.D.
APPLICANT: Liberator, P.A.
APPLICANT: Liberator, P.A.
APPLICANT: Profous-Juchelka, H.
TITLE OF INVENTION: Eimeria Brunetti DNA
TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREE: De Lincoln Avenue CITY: Rahway
                                                                                                                                                                          ADDRESSEE: Merck & Co., Inc. STREET: 126 Lincoln Avenue
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                                                                                                                                                                                             STREET: 126 Lincoln Av
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
21P: 07065
COMPUTER READABLE FORM:
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ADDRESSEE: Merck & C
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COUNTRY: USA
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US-07-879-584A-27
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                                                                      79.0%; Score 15.8; DB 1; Length 1749; 89.5%; Pred. No. 43; Live 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chakraborty, P.R.
APPLICANT: Dashkevicz, M.
APPLICANT: Elbrecht, A.
APPLICANT: Feighner, S.D.
APPLICANT: Liberator, P.A.
APPLICANT: Drofous-Juchelka, H.
TITLE OF INVENTION: Fineria Praecox DNA
TITLE OF INVENTION: Probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,594A
FILING DATE: 19920512
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19920512
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,360
FILING DATE: 29-MAY-1991
ATTORNEY/AGGNT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
                                                                                                                                                                                                                                                        RESULT 13
US-07-879-594A-27/C
Sequence 27, Application US/07879594A
Patent No. 5449768
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Merck & Co., Inc. STREET: 126 Lincoln Avenue
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TELECOMBUNICATION:
TELEPHONE: (908) 594-4720
                                                                                                                                                                                Db 1505 ATTACCCACGCCCATGGG 1487
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LENGTH: 1749 bases
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Best Local Similarity 89.55
Matches 17; Conservative
                                                                            Query Match 79.0°
Best Local Similarity 89.5°
Matches 17; Conservative
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TELEX: 138825
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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STATE: New Jersey
COUNTRY: USA
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linear
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; TOPOLOGY:
US-07-879-640A-27
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89.5%; Pred. No. 43;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,3.50 inch,800 Kb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chakraborty, P.R.
APPLICANT: Dashkevicz, M.
APPLICANT: Elbrecht, A.
APPLICANT: Feighnert, S.D.
APPLICANT: Lebrator, P.A.
APPLICANT: Lebrator, P.A.
APPLICANT: Lebrator, P.A.
APPLICANT: Droberator, P.A.
APPLICANT: Proberator, P.A.
APPLICANT: Proberator, Probes
NUMBER OF INVENTION: Probes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.4
SOFTWARE: Microsoft Word 4.0
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,640A
FILING DATE: 19920512
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/706,355
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 184211A
TELECOMINICATION INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-4720
TELEFAX: (908) 594-4720
TELEFAX: 138925
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                       NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 184181A
TELECOMMUNICATION INFORMATION:
TELEPRONE: (908) 594-5321
TELERAX: (908) 594-4720
TELERX: (908) 594-4720
TELERX: 138825
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1749 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/07879640A Patent No. 5359050 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herck & Co., Inc. 126 Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 1505 ATTACCCACGCCCATCGG 1487
      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1749 bases
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                                                                                                                                                                                                                                                                     linear
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STREET: 126 Li
CITY: Rahway
STATE: New Jer
COUNTRY: USA
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US-07-879-640A-27/C
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US-07-879-644A-27
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Search completed: February 20, 2002, 07:44:50 Job time: 198 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.0%; Score 15.8; DB 1; Length 1749; 89.5%; Pred. No. 43; ttive 0; Mismatches 2; Indels 0
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                                                                                                                                                                                            APPLICANT: Chakraborty, P.R.
APPLICANT: Dashkevicz, M.
APPLICANT: Blarecht, A.
APPLICANT: Elbrecht, A.
APPLICANT: Feighner, S.D.
APPLICANT: Liberator, P.A.
APPLICANT: Profous-Juchelka, H.
TITLE OF INVENTION: Eineria Tenella DNA
TITLE OF INVENTION: Probes
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: .184241A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19920512
CLASSIFCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/706,362
FILING DATE: 29-MAY-1991
ATTORNEY/AGENT INFORMATION:
RESULT 14
US-07-879-469A-27/c
Sequence 27, Application US/07879469A;
Patent No. 5563256
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Sequence 17, Application US/08162809
: Patent No. 5457048
: GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 89.5
Matches 17; Conservative
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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CITY: Rahway
STATE: New Jersey
COUNTRY: USA
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US-07-879-469A-27
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                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
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); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 79.0%; Score 15.8; Best Local Similarity 89.5%; Pred. No. 44 Matches 17; Conservative 0; Mismatche
                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NIMBER: 31,815
RERERENCE/POEKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
CITY: San Diego
STATE: California
COUNTRY: United States of America
21P: 92122
                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4049 base pairs
TYPE: nucleic acid
STRANDENDESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 3686 ATTCCCCACCCCCCGGG 3668
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; LOCATION: 10..2994
US-08-162-809-17
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HS_5502_A HVSMEG000 601867918 601347075

HV_CEb000 Tetraodon

602133981

602242122 Tetraodon

sa33h12.x BB542990 MR0-HT055

UI-M-AKO-UI-R-BT1fr69c02.x 1M0361D20

BB340755 BB262777

AV300572

BB334119

qt62a10.x ti33d02.x tc12f07.x UI-R-CM0-UI-R-CM0-

Post-processing:

Database

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Total number

Searched:

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AZ914287 RPC1-24-1
BF816874 MR2-CI012
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 353)
NIH MGC http://mgc.nci.nih.gov/.
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                    BG386035 353 bp mRNA EST 12-MAR-2001
602455204F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583473 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Conteat: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC
CONA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Arrayed by: The I.M.A.G.F. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.F. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1307 row: h column: 02
High quality Sequence stop: 276.
               AA954701 C
BF623736 H
AQ744329 H
BG344434 H
BF506544 G
BE560757 G
BF576543 G
                                                                                   AL200771 T
BF973134 6
AL263588 T
                                                                                                             A1443583 SBB542990 BBC708017 NBB34119 BB340755 BB340777 BB340755
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AI837244 U
AW529603 U
                                                                                                                                                                                          BI428911
AZ514882
AZ242345
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BI428911
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BF205344
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BG386035.1 GI:13279481
100
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                        RESULT
BC386035
                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
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44
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AW588384 Pa12e03.7
BE956843 601659019
BE970922 601680096
BF38368 602034011
AZ194055 SP_1025_B
BE664213 184527 MA
AW155439 Mg1e00170
BF106598 601823238
BE26683 HV_CED001
BF964059 PW4-NN120
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                                                              Search time 3814.84 Seconds (without alignments) 56.337 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                              22703874
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                              11351937 seqs, 5372889281 residues
                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                 ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                               February 20, 2002, 10:25:45
                                                                                                                                                                                                                          Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BESS 843
BEST 1922
BF 338 368
AZ 194 055
BESS 842 13
AW 1055 98
BF 1055 98
BEST 168 83
BF 964 059
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AW588384

    nucleic search, using sw model

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID
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                                                                                                US-09-904-420A-8
20
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Maximum DB seq length: 200000000
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em_gss_inv:*
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em_gss_rod:*
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Match Length DB
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gb_htc:*
gb_gss:*
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em_estom:*
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17.4 17.4 17

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Gaps

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2; Indels

Length 273;

4 others

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/lab_host="E." (coli, Xi-1 Blue MRF' (Stratagene);
/note="vector: Lambda Uni-ZAP XK Vector (Stratagene);
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library from L3 worms isolated from dog. coNA was
contructed and cloned unidirectionally into the vector
from the EcoRI to the Xhoi site. The library went
through one round of amplification."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 435)
MCCATEL, J. Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T. McCater, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T. Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Glbbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Walerston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukāryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The library was constructed by Dr. John Hawdon of Yale University (john hawdon@yale.edu). DNA Sequencing by: Washington University Genome Sequencing Center, St. Louis.
Seq primer: -4ORP from Gibco.
High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW588384 435 bp mRNA EST 10-MAY-2001
pal2e03.yl Hawdon Ancylostoma caninum L3 Ancylostoma caninum CDNA
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, Fel: 314 286 1800
Fex: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.4; DB 10;
Pred. No. 2.1e+03;
0; Mismatches 1;
                                                                                                                                                                      90.0%; Score 18; DB 10;
90.0%; Pred. No. 1.3e+03;
Live 0; Mismatches 2.
                                                               59
                                                                                                                                                                                                                                                                                                                    AW588384.1 GI:7275416
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5', mRNA sequence.
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Matches 18; Conserv
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DEFINITION
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ORGANISM
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JOURNAL
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(E. (bases 1 to 273)

Radams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A., Bult

(C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

(C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

(C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

(C.J., Lee, N.H., Kirkness, E.F., Meinstock, K.G., Gocayne, J.D., White

(C.J., Lee, N.H., Kirkness, E.F., Medblom, S., Hine, L.D., Fitzgerald

(C.J., Liu, L.I., Marnaros, S.M., Merrick, J.M.,

Kalley, J.C., Liu, L.I., Marnaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Ngyyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Kyder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, P.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Colema, T.A., Nozak, D.L.,

Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,

Weil, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon

W. R., Rosen, C.A., Hassiltine, W.A., Flelds, C., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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               /note-"Organ: colon; Vector: poTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5′ adaptor: GGCAGGAG(O.). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
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/cell_type="T-lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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nes 20; Conservative
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KEYWORDS

VERSION SOURCE

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Gaps

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Indels

Length 435;

FEATURES

TITLE

DEFINITION

ACCESSION

VERSION

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE JOURNAL

REFERENCE

BE965843/c

RESULT

qq

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E nomental principal producement: David N. Louis, M.D. Email: cgapbs-r@mail.nh.gov rissue Procurement: David N. Louis, M.D. Email: cgapbs-r@mail.nh.gov robMa.library Preparation: Life Pechnologies, Inc. cDMA.Library Preparation: Life Pechnologies, Inc. cDMA.Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 03 High quality sequence stop: 705.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                       Email: cgapbs-remail.nlh.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratoriem (LLNL)
DNA Sequencing by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMB16 row: p column: 24
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.0%; Score 17; DB 11; Length 350; 100.0%; Pred. No. 3.1e+03; .ive 0; Mismatches 0; Indels
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism~"Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="epithelioid carcinoma"
//lab_host="DH10B (phage-resistant)"
/note="Grgan: pancreas; Vector: pcMv-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 350)

NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                         BE965843 1735 bp mRNA EST 14-DEC-2000 601659019R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895660 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE970922 350 bp mRNA EST 04-0CT-2000 601680096R1 NIH_MGC_78 Homo sapiens CDNA clone IMAGE:3950471 3'
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/db_xref="taxon:9606"
/clone="IMAGE:3895660"
/clone_lib="NIH_MGC_70"
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BE970922
BE970922.1 GI:10583855
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          220 TTACCCACCCCCACGGGA 202
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BE965843
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Best Local Similarity
Matches 18; Conserv
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human.

ORGANISM

AUTHORS TITLE JOURNAL

REFERENCE

LOCUS

ACCESSION

VERSION KEYWORDS

BE970922/c

RESULT

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BASE COUNT ORIGIN

FEATURES

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Gaps

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us-09-904-420a-8.rst

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AW155439 880 bp mRNA EST 03-NOV-1999 mgie0017017f Rice blast infection stage cDNA library Oryza sativa/Pyricularia oryzae mixed EST library cDNA clone mgie0017017f AW155439.1 G1:6224308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
V0980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                         (bases 1 to 542)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from day 20 and day 40
                                                                                                      25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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                                                                                                        BE684213 542 bp mRNA EST 2
184527 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
BE684213
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Oryza sativa/Pyricularia oryzae mixed EST library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL.
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TT = 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
84.0%; Score 16.8; DB 10;
Best Local Similarity 90.0%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 2;
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/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: E column: 16
Seq primer: ATTTAGGTCACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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223 ACTACCCTCCCCCTCGGGA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·,
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Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Eukaryota; Metazoa; Echinodeae; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 489)
2 (maron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A. J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and Hood, L.
       /clone_lib="NCI_CGAP_Brn64"
//tissue_type="glioblastcma with EGFR amplification"
//lab_host="DH10B (T1 papeg-resistant)"
//note="Organ: brain: Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1:57 kb. Constructed by Life
Average insert this is a NCI_CGAP Library."

3 337 c 222 g 175 t
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AZ194055.1 GI:8377234
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/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
20402566
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                                                                                                                                                                                                                                                         85.0%; Score 17; DB 11; Length 866; 100.0%; Pred. No. 2.8e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
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Pred. No. 3.6e+03;
0; Mismatches 2;
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California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Bmail: acameron@caltech.edu
Plate: 1025 row: H column: 9
Seq primer: SP6
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Location/Qualifiers
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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Gaps

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Length 896;

us-09-904-420a-8.rst

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/clone_lib="NIH_MGC_77"
/lab_host="helioB (Tl phage-resistant)"
/lab_host="helioB (Tl phage-resistant)"
/note="organ: lung: Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGCCAATATGGC-3' and 3' (where B = A,
C', or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE216883 969 bp mRNA EST 09-MAR-2001 HV_CEb0011P02f Hordeum vulgare seedling green leaf EST library WrobNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone: HV_CEb0011P02f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 969)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,Y., Saski,C., Schwartzbeck,J., Simmons,J., Chol,D.W., Main,D. and Wood,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                   84.0%; Score 16.8; DB 11; 90.0%; Pred. No. 3.3e+03; tive 0; Mismatches 2;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Pax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Seg primer: ATTAACCCTACTAAGGG
High quality sequence stop: 530.
Location/Qualifiers
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Best Local Similarity
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BE216883
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/db_xrel=taxon:105664"
/clone="mgie0017017f"
/clone_lib="Rice blast infection stage cDNA library"
/clone_lib="Rice blast infection stage at 48 hour post-inoculation"
/note="Vector: pBlueScriptII SK(+) Vector: Rice
blast-infected leaves at 48 hour post-inoculation mRNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                   Eukaryota; mixed EST libraries.

1 (bases 1 to 880)

Rauyaree, R., Choi, W. and Dean, R.A.

Identification and characterization of genes expressed by the rice blast pathogen and rice during infection stage
Contact: Dean, R.A.

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University
Tel: 864 656 5737

Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 896) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF106598 896 bp mRNA EST 19-OCT-2000 601823238R1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4043264 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.0%; Score 16.8; DB 10; Length 880; 90.0%; Pred. No. 3.3e+03; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 others
                                                                                                                                                                                                                                                                                                                                                        Seq primer: T3 primer (AATTAACCCTCACTAAAGGG)
High quality sequence stop: 60.
Location/Qualifiers
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239 c 202 g 225 t
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/db_xref="taxon:9606"
/clone="IMAGE:4043264"
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                                                                                                                                                                                                                                                                                                                                        Email: rdean@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="70-15"
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house mouse.
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Faz: +55-11-27074322
Faz: +55-11-270704322
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4.NN1209-
231200-010-e07&t3=2000-12-23&t4=1)
Seq primer: puc 18 forward
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 261.
Location/Qualifiers
1. 281
/ Capanism="Homo sapiens"
/ Ab_xref="taxon:9606"
/ Clond_lib="NN1209"
/ Ab_xref="taxon:9606"
/ Clond_lib="NN1209"
/ Ab_xref="taxon:9606"
/ Clond_lib="NN1209"
/ Ab_xref="day"
/ Anote="Organ: nervous_normal; Vector: puci8; Site_1: Smal;
Site_2: Smal: A mini-library was made by cloning products
derived from ORESTES POR (U. S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
Profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
low stringency conditions."

57 a 50 c 59 g 115 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 281)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Rodai,M.A., da Silva,W. Jr., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

Singson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
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PM4-NN1209-231200-010-e07 NN1209 Homo sapiens CDNA, mRNA sequence.
BF964059 GI:12381334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                            Gaps
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                    Length 969;
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20202663
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               84.0%; Score 16.8; DB 10;
90.0%; Pred. No. 3.3e+03;
Live 0; Mismatches 2;
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Pred. No. 5.4e+03;
); Mismatches 1;
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94.4%;
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Matches 18; Conservative
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Martan, John M. Hiller, L. Allen, M., Bowles, M., Dietrich, M. Dietrich, M. Martan, J. Martan, M., Mobuque, T., Geisel, S., Kucaba, T., Lacy, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. Morse, M. Mouse EST Project
Unpublished (1996)

LO Contact: Martan M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Stratagene mouse embryonic carcinoma (#937317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota: Metazoa: Chordata; Craniata; VerLebrata; Euteleostomi;
Mammalia; Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 368)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Reck,C., Wylie,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:377151
                      ms64d04.rl Stratagene mouse embryonic carcinoma (#937317) Mus musculus cDNA clone IMAGE:616327 5', mRNA sequence.
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A1640019.1 GI:4703128
12-FEB-1997
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  EST
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:616327"
  mRNA
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367 bp
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Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Emmert.Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                           Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
451 314 286 1800
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA954701 448 bp mRNA EST 07-JUL-1998 OO84a06.sl NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572850 3',
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter.E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:616327"
/clone_lib="Stratagene mouse embryonic carcinoma (#937317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 448) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                             Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'tissue_type="carcinoma"
                                                                                                                                                                                                                                                                                                                                                                                     correct orientation)
MGI:377151
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .368
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Unpublished (1997)
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AA954701
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MUSNICB

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HSTCF1A AK023286 HUMMPF

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Homo sapi

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08-JUN-1995

MUSNICB 740 bp mRNA ROD Mus musculus 125 kDa nicein (NicBl) mRNA sequence. L20476 GI:854646

LOCUS DEFINITION

RESULT MUSNICB

ORGANISM

VERSION KEYWORDS SOURCE ACCESS ION

REFERENCE AUTHORS

ALIGNMENTS

Homo sapi

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Search time 1729.17 Seconds (without alignments)
133.567 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 (bases 1 to 740) Aberdam,D., Aguzzi,A., Baudoin,C., Galliano,M.F., Ortonne,J.P. and Meneguzzi,G. laminin, nicein.

Mus musculus strain C57BL/C cDNA to mRNA.

Mus musculus strain C57BL/C cDNA to mRNA.

Mus musculus strain C57BL/C cDNA to mRNA.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (basea; 1 to 740)

Aberdam, D., Galliano, M.F., Mattei, M.G., Pisani-Spadafora, A.,

Ortonne, J.P. and Meneguzzi, G.

Ortonne, J.P. and Meneguzzi, G.

Mamm. Genome 5 (4), 229-233 (1994) TITLE JOURNAL MEDLINE REFERENCE AUTHORS

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Homo sapiens
Butazota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1165)
Mayor.K., Wolff, E., Clevers, H. and Ballhausen, W.G.
The human high mobility group (HMG)-box transcription factor TCF-1: novel isoforms due to alternative splicing and usage of a new exon
                                                                                                                                                                                                                                                                                                                                                     /trānslation="MYKETVYSAFNLLMHYPPPSGAGOHPQPOPLHKANOPPHGVPO
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Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
Location/Oualifiers
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H.sapiens TCF-1 mRNA for T cell factor 1 splice form E.
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100.0%; Pred. No. 5.6e+02;
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Aberdam,D.
Submitted (102-MAY-1994) Daniel Aberdam, Faculte de Medicine, INSREM U385, Ave de Valombrose 06107, Nice Cedex 2, France on Jun 8, 1995 this sequence version replaced 9::833764.
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butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1115)
Mayer.K., Wolff, E., Clevers, H. and Ballhausen, W.G.
The human high mobility group (HMG)-box transcription factor TCF-1:
novel isoforms due to alternative splicing and usage of a new exon
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    Developmental expression of nicein adhesion protein (laminin-5) subunits suggests multiple morphogenic roles Cell Adhes. Commun. 2 (2), 115-129 (1994) 94363405
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Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
Location/Qualifiers
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2 (bases 1 to 1115)

Sujjkerbuijk,R., Geurts van Kessel,A. and Clevers,H.

The human T cell transcription factor-1 gene. Structure,
1. Biol. Chem. 267 (12), 8530-8536 (1992)
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Ballhausen, W.G.
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Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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(bases 1 to 1254)
van de Wetering,M.
Direct Submission
Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht, The Netherlands
                                                                                       Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 18 Row: d Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
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van de Wetering,M., Oosterwegel,M., Dooijes,D. and Clevers,H.
Identification and cloning of TCP-1, a T lymphocyte-specific
transcription factor containing a sequence-specific HMG box
EMBO J. 10 (1), 123-132 (1991)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Unknown (protein for IMAGE:3505629)"
/protein_id="AAH06119.1"
/db_xref="GI:13543961"
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Human TCF-1 mRNA for T cell factor 1 (splice form A).
X59869 X55327
X59869.1 G1:36785
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100.0%; Pred. No. 5.5e+02;
ive 0; Mismatches 0;
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1..1254
                                                                                                                                                                                                                                                      1. 1250
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/note="Vector: poTB7"
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Location/Qualifiers
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/codon_start=3
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Best Local Similarity 100.0%;
Matches 14; Conservative 0
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/qene="TCF-1"
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                                                                                                                                                                                                                                                                                                                                                /product_T_cell factor 1 splice form E"
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LMLGSGVPGHPAAIPHPAIVPPSGKQELQPFDRNLKTQAESKAEKEAKKPTIKKPLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FMLYMKEMRAKVIAECTLKESAAINQILGRRWHALSRĒEGAKYYELARKERQLHMQLY
PGWSARDBYGKKRRRSREKHQESTTDEGSPRKCRARRGLNOQTDWGGPCRKKKOIRY
LPGEGRCPSPVPSDDSALGGFGSPRAPPODSPSYHLLPRFPTELLTSPAERHLHPOVSPL
ISASOPGGFHRPAAPCRAHRYSDNRILRDRRPRFRFIFGRLOEPP
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                                                                                       /standard_name="T cell factor 1 splice form E"
/citation=[1]
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1250)
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Submitted (02-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Homo sapiens, clone IMAGE:3505629, mRNA, partial cds.
BC006119
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI.NL.)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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422 c 286 g 178 t
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    /cell_type="T-lymophocyte"
/cell_line="Jurkat"
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Tissue Procurement: ATCC
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                                                                                                                                                                                                               /gene="TCF-1"
                                                                          /qene="TCF-1"
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Matches 14; Conservative
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BC006119/c
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AAPLDGVLANPPNISSLSPROLLGFPCAEVSGI.STERVRELAVALAOKNVKLSTEOI.R
                                                                                                                                                                    Direct Submission Submission Submitted (23-FEB-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo Submitted (23-FEB-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo Laboratories; 1-135 Komakado, Gotemba-shi, Shizuoka prefecture 412, Japan (Tel:550-87-3411, Fax:550-87-5397)
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Human mRNA for pre-pro-megakaryocyte potentiating factor, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPF; megakaryocyte potentiating factor.
Homo sapiens pancreatic cancer cell cell_line:HPC-Y5 cDNA to mRNA,
clone:pKPO27.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates: Catarrhini; Hominidae; Homo.
1 (bases 11 to 2093)
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529. 1008
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                                                                                                                              /note="unnamed protein
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Unpublished (1996)
3 (bases 1 to 2093)
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RS 1909al.T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagal,K., Sugano,S., Shiratori,A., Sudo,H.,
Nagatsuma,M., Takahashi,M., (Chiba,Y., Kondo,H.,
Sugawara,M., Takahashi,M., (Chiba,Y., Ishida,S., Murakami,K.,
Sugawara,M., Takahashi,M., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawal,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Ishii,S., Kawal,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagathi,K., Masuho,Y., Ninomiya,K. and Iwayanayi,T.
Nakamura,Y., Nagathi,K., Masuho,Y., Ninomiya,K. and Iwayanayi,T.
Nabo human cDNA Sequencing project
Upublished (2000)

RS 1sogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AuG-2000) to the DDBJ/EMRI,GenBank datahases. Takao
Submitted (23-AuG-2000) to the DDBJ/EMRI,GenBank datahases.
Tesisla, Haya-29-0812, Japan (E-mail:genomics@hri.co.jp,
Tel:81-438-52-3951, Fax:81-438-52-3952)
NEDO human cDNA Sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
Sequencing: Research Association for Biotechnology: Chilarry
Construction, 5'-6'3'-end one pass sequencing and clone selection:
Hellx Research Institute (Supported by Japan Key Technology Center
Hellx and Japan Land and Japan Key Technology Center
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Hellx and Japan Land Japan Key Technology Center
Hellx And Japan Key Japan Key Technology Center
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligo capping; fis (full insert sequence).
Homo sapiens ovary, tumor tissue cDNA to mRNA, clone_lib:OVARC1
clone:OVARC1000008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK023286 1630 bp mRNA PRI 29-SEP-2000
Homo sapiens cDNA FLJ13224 fis, clone OVARC1000008.
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100.0%; Pred. No. 5.5e+02;
w.cmmtches 0;
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391 c 335 g 208 t
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/organism="Homo sapiens"
                           /evidence=experimental
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810
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                                                                                                                                /codon_start=1
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/gene="TCF-1"
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                                                                                                       /gene="TCF-1"
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota: Letheria; Primates; Catarrhini; Hominidae; Homo.

Thases I to 2130.

S I (bases I to 2120.

S Yamaguchi, M., Kojima, T., Ooeda, M. and Hattori, A. GENE CODING MAGARARYOCYTE AMPLIFIER

A Letter: JP 1942425767-A 1 16-AUG-1994;

CHUGAI PHARMACRUT CO LTD

OS Homo sapiens (human)

PN 19-194225767-A/1

PD 16-AUG-1994

PF 25-OCT-1993 JP 1993288617

PR 23-OCT-1993 JP 1992288617

PR 23-OCT-1992 JP 92P 329546

D9-DEC-1992 JP 92P 329546

PP 25-OCT-1992 JP 92P 329546

PP 25-OCT-1992 JP 92P 329546

PP 25-OCT-1992 JP 92P 319546
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SPEELSSVPPSSIWAVRPQDLDTCDPRQLDVLYPKARLAFONMNGSEYFVK 10SFLGG
APTEDLKALSQQNVSMDLATFMKLRTDAVLPLTVARVQKLGGPHYEGLKAEERHRPVR
DWLLBQRQDDLDTLGLGLGGGGIPNGYLVLDLSVQETLSGTPCLLGPGPVLTVLALLLA
STLA"
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: (C12N1/21,C12R1:19),(C12N5/10,C12R1:91),(C12P21/02,C12R1:19),
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/product="mesothelin"
193. .978
//note="encodes putative cleaved N-terminal portion of
mesothelin"
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CDNA encoding a polypeptide having megakaryocyte potentiating
                                                                                                                                                                                                                                                         799. 1983
/note="encodes putative membrane bound portion of maschelin, bearing epitope(s) recognized by MAb Kl" 1888. 1983
/note="encodes putative hydrophobic region for GPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2114;
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100.0%; Pred. No. 5.2e+02;
iive 0; Mismatches 0;
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topology: Linear;
hypothetical: No;
anti-sense: No;
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/note="putative"
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PLGGVLTTPINISSLSPROLLGFPCAEVSGLSTERFSRITKANVALAOKNWKLSTROLRCL
PLGGVLTTPINISSLSPROLLGFPCAEVSGLSTERFSRITKANVALLPRGAPEROR
LAPALAGEWGYRGSLLESADVRALGGLACOLPGRFVAESARVILPRLVSCPGPLODOOO
EAARAALQGGGPPYCPPSTWSVSTWALRGLLPVLGQPIRSIPTOGIVAWRRORSSRD
PSWOPERTILIEPRREVEKTACPSGKRAREIDESLIFYKKWELEACVDAALLATOW
DRVNALPFYEQLDVLKKLDELPQGYPESVIQHLGYLFLKMSPEDIRKWNYTSLET
LKALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGOLDKDTLDTLTAFYPGYICSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (09-NOV-1995) Kai Chang, Laboratory of Molecular Biology,
National Cancer Institute, Building 37, Room 4B19, 37 Convent
Drive, MSC4255, Bethesda, MD MD20892-4255, USA
Location/Qualifiers
                                                                                                                      ETIKALLEVNKGHENEPOVATLIDREVKGRGQLDKOTLDTUTAFYPGYLCSLSEBELS
SVPPSSIWAYRPODLOTCDPROLDVLYPKARLAFONNNGSEYFVKIOSFLGGAPTEDL
KALSQONVSKDLATPKKLRTDAVLPLTVAEVOKLLGPHVEGLKAEERHRPVRDWILRO
RODDLOTLGLGLQGGIPNGYLVLDLSVQEALSGTPCLLGPFVTVLALLLASTLA"
192. 950
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                     CLAHRISEPPEDLDALFLDLILETINPDAFSGPQACTRFFSR1TKANVDLLPRGAPERO RLLPAALACWGVRSLLSEADVRALGGLACDIPGRFRVASCAEVLDRYLVSGPPDLDQD OOGAARAALGGGGPPYGPSTWWSVSYMDALRGLLPVLGOP1 IFST PGG I VAANRORSS RDPSRROVERSTILERRFREVERTVACFSGKRARELDESLIFYKWHELEACVDAALLAT OWDRYNA IPFTY BOLDVLKHKLDELYPGGYPESVIQHLGYLFKWHSELDSTKWNYTSL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (Asses 1 to 2114)

Chang, K. and Pastan, I.

Molecular cloning of mesothelin, a differentiation antigen present
on mesothelium, mesotheliomas, and ovarian cancers

Proc. Natl. Acad. Sci. U.S.A. 93 (1), 136-140 (1996)
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Human mesothelin or CAKl antigen precursor mRNA, complete cds.
U40434
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/cell_type="HeLa"
issue_type="ovarian cancers and squamous cell
carcinoma."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="mesothelin or CAK1 antigen precursor"
/protein_id="AAC50348.1"
/db_xref="GI:1145724"
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                            /product."megakaryocyte potentiating factor" 2062. 2067
                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 14; DB 9; Length 2093; 100.0%; Pred. No. 5.2e+02; ive 0; Mismatches 0; Indels (
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/organiam="Homo sapiens"
/db_xref="taxon:9606"
/clone="pcb3Gxk1-9"
/chromosome="16"
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/codon_start=1
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97. .1965
/product='polypeptide having megakaryocyte
potentiating
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Pastan, I. and Chang, K.
Mesothelium antigen and methods and kits for targeting it
Patent: US 6083502-A 1 04-JUL-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                       0;
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0
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                                                                                                                                                                                                                                Length 2129;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2129)
Yamaguchi, N., Kojima, T., Oh-eda, M. and Hattori, K.
DNA coding for megakaryocyte potentiator
Patent: US 572318-A 34 03-MAR-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                PAT
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                                                                                                                                                                                                                            Query Match 100.0%; Score 14; DB 6; I. Best Local Similarity 100.0%; Pred. No. 5.1e+02; Matches 14; Conservative 0; Mismatches 0;
                                                                                                                       clone pKPO21 is A'
/clone='pKP027'
                                                                                                                               Location/Qualifiers
1. 2129
7. Organism-"Homo sapiens"
7db_xref="taxon:9606"
a 716 c 657 g 367
                                                                                                                                                                                 367
                                                                                                                                                                                                                                                                                                                                                                           US 5723318.
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Sequence 1 from patent US 6083502.
AR100763
                                                             activity,
1966. .2129
                                                                                                          in other
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716 c 657 g
                                                                                   1873
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Sequence 34 from patent
189985
189985.1 GI:3409925
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Best Local Similarity 100.
Matches 14: Conservative
                                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.
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             5'UTR
                                                                       3'UTR
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                        CDS
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ORGANISM
                                                                                                                                                source
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AR100763
LOCUS
DEFINITION
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                                                                                                                                                                                BASE COUNT
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189985
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TITLE
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VERSION
KEYWORDS
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TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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Unclassified.

1 (bases 1 to 2138)

Pastan,I. and Chang,K.
Nucleic acid encoding mesothelin, a differentiation antigen present on mesothelium, mesothelium, and ovarian cancers
Patent: US 6153430-A 1 28-NOV-2000;
Localion/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2162)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC009272 2162 bp mRNA PRI 12-JUL-2001
Homo sapiens, clone MGC:10273 IMAGE:3957372, mRNA, complete cds.
BC009272
                                                                                                                                                                          Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MAS Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
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                                                                                                                   100.0%; Score 14; DB 6; Length 2138; 100.0%; Pred. No. 5.1e+02; Live 0; Mismatches 0; Indels
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 14; DB 6; I
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0;
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                          370
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Sequence 1 from patent US 6153430.
AR119934
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722 c 661 q
                            661 g
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LAHRLSEPPEDLDALPLDLLLEUPDAFSCBPQACFTFRYBLYGWVDLLrgABPFRQR
LAAALACWGVRGSLLSEADVRALGGLACDIPGRFVAESABVLLPRLVSGPPGPLUQDO
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QEBARRAALGGGPPYGDPSTWSVSTWALBCGVFREI DFSL 1 PYKKWATLATQ
DPSWRQPPST 1 LBAFRKREVFRT ACGSGFROT 1 RS 1 PGG 1 VAAWRQRSS
TLAALLEVWKGHBWSPOVATLIDRFVKGRGGLIGNT1 AFYPGYLCSLSPEELSS
VPPSS 1 WAVRPQDLDTCDPRQLDVLYPKARLAFQWMSS PFY W 1 OSFIGGAPPFEDI.K
ALSQNVSWDLAATDWKLRTPAAVDVLPLTVAEVQKLLGPHVEGIRABERHREVRDW 1 I RQR
QDDLDTLGGGLGGGGI PWCTLVLLLSVGRALGGPVI I VLAILLASTLA "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL plate: 13 Row: a Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1129078. Location/Qualifiers
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Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 2589)
                                                                                                                                                                                                                                                                                    Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Staven Jones, Jennifer Asano, Ian Bosdet, Erin Garland, Ran Guin, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hislao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Sen Lee, Victor Ling, Carrie Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa mRNA for hypothetical protein (5'; clone 108).
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1...243
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/db_xref="taxon:9606"
/clone="MGC:10686 IMAGE:3611296"
/tissue_type="pancreas, adenocarcinoma"
/clone_lib="NIH_MGC.39"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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ilarity 100.0%; Pred. No. 5.1e+02;
Conservative 0; Mismatches 0;
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/db_xref="G1:13097582"
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Matches 14; Conserv
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VERSION
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ORIGIN
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                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Contact: wetherby.K.D., Beckstrom.Sternberg.S.M.,
Benjamin.B., Blakesley, R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan.X., Gupta.J., Ho.S.-L., Karlins.E., Legaspl.R.,
Imi,M., Waduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelenstomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (20-FEB-2001) National Institutes of Health, Mammalian
Submitted (20-FEB-2001) Cancer Genomics Office, National Cancer
Gene Collection (MCC), Cancer Genomics Office, Mational Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC003512 2433 bp mRNA PRI 12-JUL-2001
Homo sapiens, mesothelin, clone MGC:10686 IMAGE:3611296, mRNA,
complete cds.
BC003512
BC003512.1 GI:13097581
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Best Local Similarity 100.0%; Score 14; DB 9; Length 21
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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/clone="MGC:10273 IMAGE:3957372"
/tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIH_MGC_21"
/lab_host="DH10B-R"
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                                                                                                                                                                                                                                                                                                                                                                Zhang, L.-H. and Green, E.D.
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AUTHORS Cirera,S., Wintero,A.K. and Fredholm,M.

TITLE MAY do we still find anonymous ESTS?
JORRNAL Mamm. Genome 11 (8), 689-693 (2000)

REPERENCE 2 (bases 1 to 2589)

AUTHORS Cirera,S.
TITLE Direct Submission

AUTHOR Cirera,S.
TOCRINICAL (12-3AN-1999) Cirera S., The Royal Veterinary and Agricultural University, Department of Animal Science and Animal Health, Division of Animal Genetics, Groennegaardsvej 3, 1870

Frederiksberg C. DENNARK
FRATURES

SOURCE /Organism="Sus scrofa"
/ ACTIONELIDE—Taxon.9823"

ACTIONELIDE—
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32.984 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligouncleotide comptiementary

to the complementary strand of a polynucleotide which comprises one of

to the s602 nucleotide sequences defined in the specification, where the

conjouncleotide comprises at least 15 nucleotides; or (b) a combination

or an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprises a 3'-end sequence complementary to the

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polynucleotide which comprises a 3'-end sequence complementary to a

conjouncleotide comprises a 1-east 15 nucleotides and the combination of

the 5'-end sequence 3'-end sequence; selected from those defined in

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primers are useful for synthesising polynucleotides,

particularly full-length cDNAs. The primers are also useful for the

chapter conditions and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

cDNAs easily without any specialised methods. AAH03618 and

AAH03633 represent human anino acid sequences; and AAH13629 to AAH13632

represent oligonucleotides, all of which are used in the exemplification
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full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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Otsuki T;
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                                                                              Claim 1; SEQ ID 16157; 2537pp + CD ROM; English.
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Sugiyama T, Wakamatsu A, Nagai K,
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Ishii S,
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set full-length cDNAs defined in the specification. Where a primer set complises: (a) an oligo-dT primer and an oligonuclectide complementary trand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the oligonucleotide which comprises a 3'-end sequence. Where the oligonucleotide which comprises a 1'-end sequence, and sequence, where the oligonucleotide comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, and sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the particularly without any specialised methods. Ant03166 to AAM13628 and AAM13633 represent human amino acid sequences; and AAM13629 to AAM13632 or AAM56593 represent human amino acid sequences; and AAM13629 to AAM13632 or AAM56593 represent human amino acid sequences; and AAM13629 to AAM13632 or AAM56000 and AAM13633 to AAM56000 and AAM13633 to AAM5600 and AAM13633 and AAM5600 and AAM13633 and AAM5600 and AAM560
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  primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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/note= "claim 6; 248 amino acid product""
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/note= "claim 1; 584 amino acid product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1630 BP; 329 A; 585 C; 466 G; 250 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Megakaryoctye potentiator; Meg-Pot; thrombocytopenia;
                                                                                                                         Claim 8; SEQ ID 17699; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Megakaryoctye potentiator (pKP027).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA063972 standard; cDNA; 2129 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the present invention.
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Best Local Similarity 100.
Matches 14; Conservative
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93WO-US01294
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                         16-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9316178-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams MD,
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                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                CAK1 antigen; mesothelin; tumour specific antigen; mesothelioma; Ovarian cancer; squamous cell cancer; gene therapy; diagnosis; ss.
                                                                                                                              DNA encoding the 584 or 248 amino acid prod. has potential use in treatment of thrombocytopenia and low platelet function.
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                                                                                                                                                                                                                                                                                                                                                                              /+tag= b
/note= "putative signal sequence for membrane
insertion"
                                                                                                                                                                          100.0%; Score 14; DB 15; Length 2129; 100.0%; Pred. No. 1.5e+02;
                                                                                            New mega:karyoctye potentiator - for potential treatment of
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/note= "variant polyadenylation signal"
                                                                                                                                                     Sequence 2129 BP; 389 A; 715 C; 658 G; 367 T; 0 other;
                                                                                                                                                                                         ;
                                                         Oh-eda M, Yamaguchi N;
                                                                                                                                                                                         0; Mismatches
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                                                                                                                Disclosure; Page 52-57; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                   Human CAK1 antigen (mesothelin) cDNA.
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
100..1986
                                                                                                                                                                                                                                                       AAT91079 standard; cDNA; 2138 BP.
              92JP-0286153.
93WO-JP01540.
                    92JP-0301387
92JP-0329546
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                                          (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                               Best Local Similarity 100.
Matches 14; Conservative
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                                                        Hattori K, Kojima T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-372620/34.
P-PSDB; AAW26674.
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                                                                                                    thrombocytopenia
                                                                              P-PSDB; AAR53992
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                    11-NOV-1992;
09-DEC-1992;
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25-OCT-1993;
              23-OCT-1992;
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                                                                                                                                                                          Query Match
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Agents for targeting mesothelin, a tumour cell antigen - used for
the detection or inhibition of growth of e.g. mesotheliomas, ovarian
cancers and squamous cell carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mesothellomas or ovarian tumours. DNA encoding the mesothelin antigen can be transfected into a mammal containing tumour cells to screen for drugs useful in cancer treatment. Antisense oligonucleotides can be used to inhibit mesothelin expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methods can be used to detect tumour cells and to inhibit the growth of cells bearing mesothelin. Mesothelin-derived antigens may be used in vaccines for the inhibition or prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene transcription product, genetic markers, tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          This cDNA clone codes for CAK1 antigen (see AAW26674) which is
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                                                                                                                                                                                                                                                                                                                    Claim 16; Page 58-60; 72pp; English.
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WO200155339-A2.
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Liu C,
                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                 library as part of a large set of ESTS which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST02392 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also AAQ59041-Q61440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer specific for DNA encoding secretory/membrane protein SEQ ID 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding secretory proteins/membrane proteins, useful in
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy or as candidate target molecules in drug development
                Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging of most human genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi
                                                                                                                      Expressed Sequence Tag was isolated from a human brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                             Score 13; DB 14; Length 347;
Pred. No. 5.5e+02;
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                                                                                                                                                                                                                                                                                           Sequence 347 BP; 76 A; 87 C; 79 G; 101 T; 4 other;
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                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                     500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishikawa T,
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ID AAF93992 standard; DNA; 650 BP.
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11-JAN-2000; 2000JP-0118775.
02-MAY-2000; 2000JP-0183766.
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289 CTGCTCCCGAGGG 277
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                                                                                     Example 4; Page 327;
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and actagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; nootropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory; gene therapy; antiense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder; netrous system disorder; inflammation; expressed sequence tag; EST; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 650 BP; 116 A; 200 C; 154 G; 170 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.9%; Score 13; DB 22; 1 100.0%; Pred. No. 5.4e+02;
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Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 656-657; 715pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human foetal cDNA, SEQ ID NO: 1163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH94476 standard; cDNA; 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000; 2000US-0491404.
15-SEP-2000; 2000US-0663870.
06-NOV-2000; 2000US-0707351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2001; 2001WO-US02723.
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Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-465571/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 cctgctcccgagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAM06801
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Gaps

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Indels

DB 20; Le 5.3e+02; hes 0;

92.9%; Score 13; DB llarity 100.0%; Pred. No. 5.3 Conservative 0; Mismatches

Query Match

Length 1147;

8888888888888

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This invention describes novel nucleic acid sequences (A) that are expressed at high level in prostatic tumor tissue and encode gene products or their fragments. The products of the invention have antitumor activity. Polypeptides (I) encoded by (A) are used: (i) for identifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to lasolate full-length genes (for gene therapy) and for recombinant production of (1), which can be used to raise specific antibodies. (A) are identified by assembly of ESTS (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTS. AAX33423-233476 represent expressed sequence tags described in the method of the invention.
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polynucleotides comprising one of 477 sequences fully defined in the specification. The foetal polynucleotides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence is a full length cDNA which was assembled using expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate tumor; antitumor; treatment;
                                                                                                                                                                                       sequence tags (ESTs) found to be expressed in human foetal tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                        Sequence 994 BP; 320 A; 205 C; 176 G; 293 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              92.9%; Score 13; DB 22; I
100.0%; Pred. No. 5.3e+02;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; tissue specificity human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate cancer-associated EST 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (META-) METAGEN GES GENOMFORSCHUNG MBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ33452 standard; cDNA; 1147 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tag; EST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                               CDNA libraries as seeds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 cctgctcccgagg 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 cctgctcccgagg 13
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es 13; Conserv
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                     gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.98; Score 13; DB 20; Length 1383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1383 BP; 337 A; 352 C; 424 G; 270 T; 0 other;
                                                                                                                                                                                              Porphorymonas gingivalis protein PG119 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 5.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Margetts MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 194; 588pp; English.
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100.08; FIE
0; F
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Webb EA;
                                                                                                                  AAX91681/c
ID AAX91681 standard; DNA; 1383 BP.
                                                                                                                                                                                                                                                                                                                                                                                      97AU-0001182.
98AU-0001546.
98AU-0002264.
98AU-0002911.
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98AU-0003338.
98AU-0003654.
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97AU-0000839.
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                                                                                                                                                                                                                                                                Porphorymonas gingivalis
                                                             1094 cctgctcccgagg 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     especially gingivitis.
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Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-385613/32
                                                                                                                                                                                                                            Porphorymonas gingivaccine; antigenic;
Best Local Similarity
Matches 13; Conserv
                                        1 cctgctcccgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY34463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CSLC-) CSL LTD.
                                                                                                                                                                                                                                                                                                                                                              04-AUG-1998;
10-DEC-1997;
30-DEC-1997;
30-JAN-1998;
10-MAR-1998;
09-APR-1998;
23-APR-1998;
22-MAY-1998;
                                                                                                                                                                                                                                                                                        W09929870-A1.
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                                                                                                                                                                                                                                                                                                               17-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agius CT,
                                                                                                                                                     AAX91681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ross BC,
                                                                                                    RESULT
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169 CCTGCTCCCGAGG 157

1 cctgctcccgagg 13

ò qq vaccine; antigenic; ds.

25-AUG-1999

AAX91557:

AAX91557/

WO9929870-A1.

10-DEC-1998;

04-AUG-1998 31-DEC-1997 30-JAN-1998 10-MAR-1998 09-APR-1998 23-APR-1998 05-MAY-1998

10-DEC-1997

17-JUN-1999

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The present sequence represents a kidney injury associated molecule (KIM) cDNA clone. KIM proteins can be administered therapeutically by expressing KIM enroding polynucleotides, to promote growth and/or survival of damaged tissue (e.g. renal tissue), since the KIM proteins are upregulated in injured or regenerating (especially renal) tissues.

KIM fusion proteins, conjugates, antibodies and vectors can also be used therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy. prophylaxis of conditions associated with disfunction/disregulation of KIM genes or proteins, especially renal diseases or impairments of renal phylaxis of conditions associated with disfunction/disregulation of KIM genes or proteins, especially renal diseases or impairments of renal internalised into cells, can disrupt expression of a cellular KIM gene, olynucleotides can be used to produce antisense sequences which, when internalised into cells, can disrupt expression of a cellular KIM gene, also useful in therapy (e.g. to block the growth of tumours dependent on KIM for growth) or compositions. The proteins and polynucleotides are useful diagnostically e.g. to detect and quantify renal injury/disease function), or abnormal responses to tissue injury (indicative of increased risk, or presence of, renal injury or impaired increased risk, or presence of, an autoimmune response or abnormal and proteins and polynucleotides are an example responses to tissue injury (indicative of increased risk, or presence of, an autoimmune response or abnormal and proteins and polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue growth arising from/affecting renal tissue). The proteins can also be used to locate KIM-producing cells (especially specific loci, e.g. tissue masses abnormally producing/expressing KIM such as tumours arising from/affecting renal tissue), by contacting cells with an imageable KIM-binding reagent and imaging reagent accumulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
                                                                                                                                                                                                          Kidney injury associated molecule; kidney injury related molecule; KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                Kidney injury associated molecule HW076 cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanicola-Nadel M, Wei H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.9%; Score 13; DB 20; 100.0%; Pred. No. 5.2e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers complement (42..281)
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/label= SAC_24409
AAV80620/c
ID AAV80620 standard; cDNA; 1668 BP.
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                                                                                                                    (first entry)
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Best Local Similarity 100.0
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-045312/04
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                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                    01-MAR-1999
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                                                                                                                                                                                                                                                                                                                      Rattus sp.
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                                                                        AAV80620;
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                            ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAAY3483. AAX34802 to AAX91899 represent PCR primers used in the lasolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines sepecially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is linvolved in periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                        Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Margetts MB, Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.9%; Score 13; DB 20; Length 1386; 100.0%; Pred. No. 5.2e+02; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                      Porphorymonas gingivalis protein PG119 ORF encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1386 BP; 338 A; 352 C; 426 G; 270 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 109; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hocking DM,
                                                                                                                                                                           AAX91557 standard; DNA; 1386 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98AU-0002911
98AU-0003128.
98AU-0003338.
98AU-0003654.
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97AU-0000839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97AU-0001182
98AU-0001546
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                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas gingivalis
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Barr IG, Rothel LJ,

Agius CT,

Ross BC,

(CSLC-) CSL LTD.

22-MAY-1998; 29-JUL-1998;

WPI; 1999-385613/32

P-PSDB; AAY34339

gingivitis

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172 CCTGCTCCCGAGG 160

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RESULT

1 cctgctcccgagg 13

especially gingivitis

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AAF60009 standard; DNA; 1954
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                                                                                                                                                                                                                                                                                            Tang YT,
Shah P,
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                                                  AAF60009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                 AAF60009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes a novel adenovirus chimeric protein, Pig4KN. This protein is used in a method for the construction of novel monomers having an N-terminus of an adenoviral fibre protein and a trimerisation domain. Such monomers have lower affinity for native substrate than the native adenoviral fibre trimer. Cell lines containing such monomers are used (1) to propagate adenovirus for use as gene therapy vectors (for in vitro or in vivo applications, (ii) as reagents for studying adenoviral attachment and infection, and (iii) in receptor-ligand interaction assays. The new viruses produce minimal ectopic infection (they can not infect native host cells) so are safer as vectors and can be engineered for selective
                                                                                                                                                             Pig4KN; chimeric protein; adenoviral fibre protein; monomer; infection; trimerisation domain; affinity; substrate; gene therapy vector; attachment; interaction assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New adenoviral fibre trimer with reduced binding to native substrate - useful for, e.g. preparing gene therapy vector with minimal ectopic infection for in vitro applications
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                                                                                                                                                                                                                                                                                                                                                                                                                      Kovesdi I, Lizonova A, Roelvink PW;
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100.0%; Pred. No. 5.2e+02;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 1830 BP; 436 A; 586 C; 425 G; 383 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 52-54; 103pp; English.
                                                                                                                                                                                                                                          Location/Qualifiers
1..1830
/*tag= a
/product= "Pig4KN"
                                                                           AAV72023 standard; DNA; 1830 BP.
                                                                                                                                                                                                                                                                                                                                            98WO-US11024.
                                                                                                                                                                                                                                                                                                                                                                98US-0071668.
97US-0047849.
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 92.9
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  targeting to other cells
                                                                                                                                                                                                                                                                                                                                                                                                                                   Yonehiro G;
                                                                                                                                                                                                                                                                                                                                                                                                                      Einfeld D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 cctgctcccgagg 13
                                                                                                                                           Adenovirus Pig4KN DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-059848/05.
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                                                                                                                                                                                                             Mastadenovirus
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                                                                                                                                                                                                                                                                                                                                            28-MAY-1998;
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                                                                                                                    29-MAR-1999
                                                                                                                                                                                                                                                                                                                       03-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                      Brough DE,
Wickham TJ,
                                                                                                                                                                                                                      Synthetic.
                                                                                                AAV72023;
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New human synthetases, useful for diagnosing, preventing and treating immune disorders, neuronal disorders, reproductive disorders, and cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human synthetase proteins. These proteins are useful for treating diseases in which they are involved. Such diseases include immune disorders such as inflammation, acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunodeficiency syndrome (AIDS), allergies, autoimmune diseases, infections cancers, Alzheimer's disease, reproductive disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopolesis; anaemia; myeloid cell deficiency; myeloid cell; esticiency; myeloid cell; esticiency; myeloid cell; erythroid progenitor cell; colony simulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet; platelet disorder; thrombocytopenia; hematopoeitic stem cell;
                                                                                                                                                                         Human; synthetase; immune; inflammation; AIDS; infection; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%; Score 13; DB 22; I 100.0%; Pred. No. 5.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 115-116; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bandman O,
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100.0%; Pre-
0; '
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BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections cancers, Alzheimer cell proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-2000; 2000WO-US19980.
                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0144992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0168858,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC.
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                                                                                        26-APR-2001 (first entry)
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                                                                                                                                   Human synthetase #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                    reproduction; ds
                                                                                                                                                                                                                                                                                            WO200107628-A2.
                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUL-1999;
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1574 cctgctcccgagg 1586

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AAZ36228-49 encode bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell deficiencies. In addition, they may be used to support the growth and proliferation of erythroid progenitor cells, and to treat various anemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myelo-supports or macrophages, to prevent or treat myelo-supports and platelets, thereby allowing prevention or treatment megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoeitic stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage and conjunction and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage dange or defects, prophylactic use in the improved fixation of artificial
stem cell disorder; aplastic anaemia; bone differentiatiou; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer; bone fracture; cartilage damaqe; artificial joint; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations -
                                                                                                                                                                                  'product= "bone marrow secreted protein"
104..304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1990 BP; 344 A; 727 C; 574 G; 345 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 114-115; 120pp; English.
                                                                                                                              Location/Qualifiers
104..1617
                                                                                                                                                                                                                                                                                                                                                                                                          97US-0068958.
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1952..1957
/*tag= c
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P-PSDB; AAY53641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cao L;
                                                                                                                                                                                                                                                                                                                                                                       18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1998;
30-SEP-1998;
                                                                                             Homo sapiens
                                                                                                                                                                                                                                            polyA_signal
                                                                                                                                                                                                                                                                                               WO9933979-A2
                                                                                                                                                                                                                                                                                                                                                                                                          10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                   08-JUL-1999
                                                                                                                                                                                                      sig_peptide
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                                                                                                                              Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New adenoviral fibre trimer with reduced binding to native substrate - useful for, e.g. preparing gene therapy vector with minimal ectopic infection for in vitro applications
                                                                                                                                         PNSPig4.SS; chimeric protein; adenoviral fibre protein; monomer; trimerisation domain; affinity; substrate; gene therapy vector; attachment; interaction assay; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Einfeld D, Kovesdi I, Lizonova A, Roelvink PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.9%; Score 13; DB 20; I
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                             "Chimeric protein"
                                                                                                                                                                                                                                                                                             "PNSpig4.SS"
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                           BP.
                           AAV72024 standard; DNA; 2253
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97US-0047849.
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                                                                                    (first entry)
                                                                                                                  Adenovirus PNSPig4.SS DNA.
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                                                                                                                                                                                                                                                                                             /product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAV72024
                                                                                                                                                                                                          Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                            W09854346-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-1998;
                                                                                    29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wickham TJ,
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                                                                                                                                                                                                                     Synthetic.
                                                         AAV72024;
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           AAV72024
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Gaps

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Score 13; DB 21; Length 1990; Pred. No. 5.2e+02; 0; Mismatches 0; Indels 0

92.9°, 100.0%; Pre-0;

Local Similarity 100. nes 13; Conservative

Matches

Query Match

1 cctgctcccgagg 13

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Search completed: February 20, 2002, 10:31:58 Job time: 10226 sec

Appli Appli

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APPLICANT: Yamaguchi, No. 57233180mi
APPLICANT: Yamaguchi, Tetsuo
APPLICANT: Oh-Eda, Masayoshi
APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Genes Coding for Megakaryocyte
TITLE OF INVENTION: Potentiator
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: C--COS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,819A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747 CITY: Falls Church STAFE: Virginia
US-08-700-636-3

US-08-467-574-3

US-09-217-345-3

US-09-110-937-1

US-09-058-725B-1

US-09-058-725B-1

US-09-232-857-1

US-09-232-857-1

US-08-629-399-1

US-08-759-873-1

US-08-759-873-1

US-08-759-873-1

US-08-775-009-36

US-08-775-009-36

US-08-775-009-36

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US-08-077-848A-1
US-09-211-640-1
US-09-378-536-1
                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MITOPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/TOCKET NUMBER: 230-107P
TELEPHONE: 703-205-8000
TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         US-08-426-819A-34
; Sequence 34, Application US/08426819A
; Patient No. 5723318
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant TOPOLOGY: not relevant
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TYPE: nucleic acid
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LOCATION: 97..1965
FEATURE:
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STATE: Virgini
COUNTRY: USA
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STRANDEDNESS:
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     CLONE:
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Sequence 1, Appl
Sequence 17, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 27, Appl
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                                                                                                                                             (without alignments)
19.007 Million cell updates/sec
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                                                                                                                           Search time 166.82 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-76-271-1
US-09-215-055-1
US-09-215-055-1
US-08-998-416-676
US-09-176-862-22
US-08-247-475-22
US-08-191-8660-22
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US-08-191-8660-22
US-08-191-8660-22
US-08-193-948-27
US-08-193-962-5
US-09-212-149-2
US-09-212-149-2
US-09-109-100-1
US-08-243-545-5
US-09-109-100-2
US-08-195-967-1
                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                               351203 seqs, 113238999 residues
                                                                                                                               February 20, 2002, 07:44:41
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Maximum Match 100%
Listing first 45 summaries
                                                                                                nucleic search, using sw model
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length: 2000000000
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Maximum DB seq
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No.
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GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Pastan, Ira
APPLICANT: Chang, Kai
TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/215,035 FILING DATE: No. 6153430 yet assigned CLASSIFICATION: PRIOR APPLICATION: PRIOR APPLICATION DATA: PFILING DATE: 01-DBC-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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100.0%; Pred. No. 36;
.ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: WO PCT/US97/00224 FILING DATE: 03-JAN-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/010,166 FILING DATE: 05-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6239264
                                                                                                                         ; Sequence 1, Application US/09215035
; Patent No. 6153430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Faris, Susan K.
REGISTATION UNBER: 41,739
REFRENCE/DOCKET NUMBER: 0152
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 100.
Matches 14; Conservative
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STRANDEDNESS: single
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STREET: Two Embarcac
CITY: San Francisco
STATE: California
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ZIP: 94111-3834
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US-08-998-416-676
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                                                                                                       US-09-215-035-1
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APPLICANT: Chang, Kai
TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
CORRESPONDENCE ADDRESS:
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                                                                                                                   100.0%; Score 14; DB 1; Length 2129; nilarity 100.0%; Pred. No. 36; Conservative 0; Mismatches 0: Trail
                  /note= "this residue is A in pKP021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,271
FILING DATE: 01-DEC-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                015280-259100US
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PRIOR APPLICATION NUMBER: WO PCT/US97/00224

FILING DATE: 03-JAN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/010,166

FILING DATE: 05-JAN-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                US-08-776-271-1
; Sequence 1. Application US/08776271
; Patent No. 6083502
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPRA: (415) 576-0200
TELEPRA: (415) 576-0300
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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100..1986
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         ; LOCATION: 1873
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-426-819A-34
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                                                                                                                                     Query Match
Best Local Similarity
Matches 14; Conserv
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94111-3834
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STREET: TWO
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Sequence 22, Application US/09176862B

; Sequence 22, Application US/09176862B

; Patent No. 6046319

; GENERAL INFORMATION:

; APPLICANT: Power, Christopher

; APPLICANT: Payne, Michael B

; TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES REGULATING EXPRESSION

; TITLE OF INVENTION: OF TNF-ALPHA

; FILE REPERENCE: 3045.00002

; CURRENT APPLICATION NUMBER: US/09/176,862B

; CURRENT FILING DATE: 1998-10-22

; EARLIER PILING DATE: 1997-10-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0
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. OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-176-862-22
                                                                                                                                                                                                                                                   92.9%; Score 13; DB 3; Length 152331;
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.6%; Score 12.4; DB 3;
illarity 92.9%; Pred. No. 2.7e+02;
Conservative 0; Mismatches 1;
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Sequence 22, Application US/08247475
Sequence 22, Application US/08247475
Sequence 22, Application US/08247475
September 1 NFORMATION:
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Infectious BC
TITLE OF INVENTION: Rehinotracheitis Virus
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STREET: New York
NUMBER OF SEQ ID NOS: 18
SCOTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
                                                                                                                                                          ; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                         Query Match 92.9
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                 1 cctgctcccgaggg 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                           FEATURE:
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APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
                  APPLICANT: Philippen, Peter
APPLICANT: Philippen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Mendland, Jurgen
APPLICANT: Mendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
APPLICANT: Reming, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STARE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09128155 Patent No. 6117654
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Best Local Similarity 100.
Matches 13; Conservative
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              GENERAL INFORMATION:
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Cochran, Mark D
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D.
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Renombinant Infectious S-IBR-052 And Uses Thereof
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                    Score 12.4; DB 1;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.6%; Score 12.4; DB 1;
92.9%; Pred. No. 2.6e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                           0; Mismatches
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FILING DATE: 4 February 1994
CLASSIFICATION: 435
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; Patent No. 5783195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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92.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                    Query Match 88.6
Best Local Similarity 92.9
Matches 13; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                     ; ANTI-SENSE:
US-08-479-650-22
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US-08-191-866D-27
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Matches
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Pred. No. 2.6e+02;
0; Mismatches 1; Indels
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ZIP: 1003

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,650
FILING DATE: June 7, 1995

TASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cochran, Mark D.
APPLICANT: Macdonald, Richard D.
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Line
TITLE OF INVENTION: Rhinotracheitis Virus
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,475
FILING DATE: May 23, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...urusSSEE: John P. White STRET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08479650
Patent No. 5599544
GENERAL INFORMATION:
                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMONICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
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                                                                                                                                                                                                                                                                                 TELEFAX: (212) 391-0525
TELER: 422523
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.6%;
92.9%;
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Matches 13; Conservative
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INFORMATION FOR SEQ ID NO:
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US-08-247-475-22
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Score 12.4; DB 2; Length 102; Pred. No. 2.6e+02; 0; Mismatches 1; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
. CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: White, John P.
RELECOMMUNICATION NUMBER: 678
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF $120.2 278-0400
TELECOMMUNICATION OF $20.2 278-0400
TELECOMMUNICATION OF $20.2 278-0505
TELECOMMUNICATION: 278-0505
SEQUENCE CHARACTERISTICS:
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Patent No. 5925543
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
TITLE OF INFUNION: NADH DEHYDROGENASE B17 SUBUNIT
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,926A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0384 US
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NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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92.9%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.6
Best Local Similarity 92.9
Matches 13; Conservative
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE:
US-08-185-949B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                       Sequence 22, Application US/08674169
; Sequence 22, Raplication US/08674169
; Patent No. 5804372
; GENERAL INFORMATION:
    APPLICANT: COCHEAN, MARK D.
; APPLICANT: Macdonald, Richard D.
; TITLE OF INVENTION: Recombinant Infectious Bovine; TITLE OF INVENTION: Recombinant Infectious Bovine; TITLE OF SEQUENCES: 51
CORRESPONDENCES: 51
CORRESPONDENCE ADDRESS:
    ADDRESSE: John P. White
    STREET: 1185 Avenue of the Americas
    CITY: New York
    STATE: New York
    COUNTRY: USA
    COUNTRY: USA
    CAMMITTEN OF AMERICAN COUNTRY: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Infectious Bovine
Rhinotracheitis Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,169
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us-u8-185-949B-27
Sequence 27, Application US/08185949B
Patent No. 584279
GENERAL INFORMATION:
GENERAL INFORMATION:
THILE OF INVENTION:
TITLE OF INVENTION: Recombinant Infection TITLE OF INVENTION: Rhinotracheltis Vir NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas CITY: New York
COUNTRY: USA
ZIP: 10076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0525
TELERA: (212) 391-0525
INFORMATION FOR SED ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
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Best Local Similarity 92.9
Matches 13; Conservative
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US-08-674-169-22
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Gaps

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APPLICANT:
APPLICANT:
TITLE OF INVENTION: Purified Mammalian Flt3 Ligands and Agonists and Antagonist
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-243-545-5/C
Sequence 5, Application US/08243545
Patent No. 5554512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
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ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.4; DB 5;
Pred. No. 2.6e+02;
0; Mismatches 1;
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FILLING DATE: 19-MAY-1993
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                         Sequence 19, Application PC/TUS9405150 GENERAL INFORMATION:
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92.9%;
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LENGTH: 857 base pairs
TYPE: nucleic acid
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CITY: Seattle
STATE: Washington
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Best Local Similarity
Matches 13; Conserv
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PCT-US94-05150-19/c
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Pred. No. 2.6e+02;
0; Mismatches 1; Indels
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Pred. No. 2.6e+02;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-212-149-2/C
Sequence 2, Application US/09212149
Fatent No. 6100036
GENERAL INFORMATION:
APPLICANT: Lal, Freeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NABH DEHYDROGENASE B17 SUBUNIT
NUMBER OF SEQUENCES:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  0; Mismatches
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APPLICATION NUMBER: 08/928,926
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 610 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.6%;
92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity 92.99
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                       TYPE: nucleic acid
STRANDEDNESS: single
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; LIBRARY: TBLYNOT01
; CLONE: 44898
US-09-212-149-2
                                                                        TOPOLOGY: linear
MMEDIATE SOURCE:
LIBRARY: TBLYNOT01
CLONE: 44898
US-08-928-926A-2
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us-09-904-420a-5.rni

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COUNTRY: US

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: MICTOSOfT WORD, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: Angust 25, 1993
CLLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: Angust 12, 1993
CLLASSIFICATION: 435
PRIOR APPLICATION: 435
FILING DATE: May 24, 1993
CLLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 24, 1993
CLLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
TELEPRAN: (206) 233-0644
TELEFAX: 756822
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERFSTICS:
LENGTH: 988 base pairs
TYPE: NUCLEIC ACID
STANDENDESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO FEATURE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: 30..734
US-08-243-545-5
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Gaps ; 88.6%; Score 12.4; DB 1; Length 988; 92.9%; Pred. No. 2.6e+02; tive 0; Mismatches 1; Indels (Query Match
Best Local Similarity 92.9
Matches 13; Conservative

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Search completed: February 20, 2002, 07:44:49 Job time: 197 sec

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AL556629 AL55629
BF127436 601567623
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A299674 2M0287C11
B1333443 602996934
A299674 2M0287C11
B1333443 6019695
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BE266940 601092425
BE900825 601674556
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A155912 A155912 A155912
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                  AL514070 AL514070
AL245817 Tetraodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                          AW463205
BF940615
                                                    AW975810 | BF194763 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Monse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tal: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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                                                                                                                 AZ617446
BF434130
AI673528
AL556629
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BE278765
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AZ704040
AL514070
               BF940593
AW463205
                                         BF940615
AW975810
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AW659550
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     ;, mRNA s
AA275661
     RESULT 1
AA275661/c
LOCUS
DEFINITION
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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                                             Bonaldo, Ph.D. Chrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NOI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llni.gov/Dbrp/image/image.html
Insert Length: 1282 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicyap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
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/db_xref="taxon:9606"
/clone='IMAGE:1301678"
/clone_lib="NCI_CGAP_GCBI"
/tissue_type="germinal center B cell"
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]. Double-stranded cDNA was liqated to Eco RI adaptors (Pharmacia), digested with Not 1 and cloned into the Not I
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information can be
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L Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at:
www-bio.llnl.gov/bbrp/Amage/image.html
Insert Length: 1310 Std Error: 0.00
Seq primer: -40ml3 fwd. Err from Amersham
High quality sequence stop: 183.
Location/Qualifiers
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_GCB1"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-25 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
Swith: http://genome-gsc.riken.go.jp,
Sasaki,N., Izawa,M., Watchiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Y. and Hayashizak',Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carnincl,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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/db_xref="taxon:10090"
/clone="5430433E23"
/clone_lib="RIKEN full-length enriched, 6 days neonate head"
and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatina Bonaldo."

49 63 9 37 Lothers
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further details.
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AV293106 RIKEN full-length enriched, 6 days neonate head Mus musculus cDNA clone 5430433E23 3', mRNA sequence.
AV293106.1 GI:6307137
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Matches 14; Conservative
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Mammalia Eutheria; Firmates; Catalinii; Nominiaes; Namo.

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Farle-Hughes, J., Fine, L.D., Fitzgerald

L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M.,

Relley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nyuyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrle, A., Fischer, C., Hastings, G.A., He, W. W.,

Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Kunsch, C., Hungjun, J., Li, H., Melsner, P.S., Olson, H., Raymond, L.,

Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Kuben, S.M., Dillion, P.J., Fannon,

W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA311787 273 bp mRNA EST 19-APR-1997 EST182503 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to similar to T-cell factor 1, A/B/C, mRNA sequence.
AA311787 GI:1964114
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9712 Medical Center Drive, Rockville, MD 20850 USA
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                           /dev_stage="6 days neonate"
/lab_host="DH10B"
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/tissue_type="head"
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Conservative 0
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1 (bases 1 to 281)

Fabrankrug, S.C.; Freking, B.A.; Rohrer, G.A.; Smith, T.P.L., Casas, E., Stone, R.T.; Heaton, M.P.; Grosse, W.M.; Bennett, G.A.; Laegreid, W.W. and Keele, J.W.

EST discovery in swine Uppublished (2000)

Contact: Smith FP.

Contact: Smith FP.
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="AATC( inhost):158998"
/db_xref="taxon:9606"
/dolo=_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
**Note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Site_2: **Note="Vector: PBluescript SK-; Site_1: EcoRI; Sk-; Site_2: **Note="Vector: PBluescript SK-; Site_2:
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17905 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW325590
AW325590.1 GI:6761511
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No Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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PORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGACG
Plate: 8 row: M column: 8
Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
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/db_xref="taxon:9823"
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/tissue_type="pooled"
/lab_host="DH10B"
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Nus musculus

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 283)

Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P.,

Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y.,

Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y.,

Hanagaki, T., Hayatsu, N., Hiraoka, T., Makamura, M., Nishi, K.,

Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C.,

Sakai, K., Sasaki, D., Sato, K., Shibata, Y., Soabe, Y., Sakai, Y., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, F., Tanaka

Shiraki, T., Soqabe, Y., Satuki, H., Taqawa, A., Takahashi, F., Tanaka

Shiraki, A., Muramatsu, M. and Hayashizaki, Y., Vasunishi, A., Yoshida, K.,

Yoshiki, A., Muramatsu, M. and Hayashizaki, Y., Sabilishi, A., Yoshida, K.,

Sciences Center(GSC), Yokohama Institute

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

In-7-25 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9216

Email: genome escirken-go.jp,

URL: http://genome.gsc.riken-go.jp,

URL: http://genome.gsc.riken-go.jp,

URL: http://genome.gsc.riken-go.jp,

URL: http://genome.gsc.riken-go.jp,

URL: http://genome.gsc.riken-go.jp,

URL: http://genome.gsc.riken-go.jp,

Thermostabilization and thermoactivation of thermolastion, Carninci, P., Nishiyama. Y., Wastover, A., Itoh, M., Nagaoka, S., Sasaki

Yokazaki, Y. Muramatsu, M. and Hayashizaki, Y.

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

10.4.4 (1999)
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/db_xref="maxon:10090"
/clone="E230006M17"
/clone=lib="RixEN full-length enriched, 2 days pregnant adult female oviduct"
/sox="female"
/tissue_type="oviduct"
/dov_stage="oviduct"
/dov_stage="2 days pregnant adult"
/lab_host="PH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                     BB607667 RIKEN full-length enriched, 2 days pregnant adult female oviduct Mus musculus cDNA clone E230006M17 5', mRNA sequence.
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp)
further details.
                                                                              6
Length 281;
    Ouery Match
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 0;
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/organism="Mus musculus"
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Contact: Yoshihide Hayashizaki
                                                                                                                                    Email: genome-resigac.riken.go.jp,
UR.:http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci.P., Nishiyama,Y., Mathagaria,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermolabile enzymes by
Crimalose and its application for the synthesis of fill length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
V. and Hayashiyaki,V. Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" GAGAGAGAGGGCGCAACTCGAGTTTTTTTTTTTVN 3'], cDNA was
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 288)
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carnincl, P. and Hayashizaki. Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB367350 288 bp mRNA EST 12-JUL-2000 BB367350 RIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone Cl30037J03 3', mRNA sequence. BB367350.1 GI:9079179
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Matches 14; Conservative
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tay present in the cDNA between the NoLI site
                                                                                                                               /clone_lib="RIKEN full-length enriched, 16 days embryo head"
our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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201 Kildee Hall, Ames, 1A 50011-3150, USA
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97044477
                                                                           /organism="Mus musculus"
                                                                                         /strain="C57BL/6J"
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/clone="C130037J03"
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                                   Location/Qualifiers
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                                                                                                                                                                                           /sex="mixed"
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 Please visit our further details.
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Tel: 5152944252
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/vigurian="crossbredge"
/db_xxef="taxon:9823"
/db_xxef="taxon:9823"
/clone_lib="Mr-P-CPI-nwr-g-11-0-UI"
/clone_lib="Mr-P-CPI-nwr-g-11-0-UI"
/clone_lib="Mr-P-CPI-nwr-g-11-0-UI"
/lab_host="DH100 (Life Technologies)" with a modified
/note="Vector: pr7730-pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_l: EcoRI; The MI-P-CPI
library is normalized library derived from the MI-P-CPI
library, ultimately derived from uterus tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.iastate.edu/. The procedure used to
create this library has been previously described (Bonaldo
.Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG_LIB=MI-P-CPI
mag_CD_spectors.
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Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

El (bases 1 to 347)

SG Grossman,A., Davies, J. Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.

Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2

Unpublished (2000)

Contact: Elizabeth H. Harris

DCMB Box 91000

Duke University

Durke University

Far: 919 613 8164

Fax: 919 613 8177
and the oligo-dT track served to verify it as a clone from the normalized diterus library oDNA Library Preparation: M.B. Soares Lab. University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research
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II"
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/strain="CC-1690 wild type mt+ 21gr"
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100.0%; Score 14; DB 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 0;
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TAG_SEQ=AGTCCAATCG"
1 86 c 91 g
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Chlamydomonas reinhardtii
                                                                                                                     Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-Yes.
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BE227885.1 GI:8933124
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/note="Vector: pBluescript II SK.; Site_I: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from Cc-1690 cells grown to
mid-log phase in TAPP (acetate-containing) medium in the
light, TAPP medium in the dark, HS (minimal) medium in
ambient levels of Co2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites,
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exhssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) genome Research 6: 791-806."
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/issue_type="adenocarcinoma ccil line"
/lab_host="DHIOH (phage-resistant)"
/note="Organ: colon: Vector: poTB7; Site_1: Xhol: Site_2:
/note="Organ: colon: Vector: poTB7; Site_1: Xhol: Site_2:
CCORI; CDNA made by oliqo-dT priming. Directionally
cloned into EcoRIXXhol sites using the following 5'
adaptor: GGACGGG(G). Size=reslected 500bp for average
insert size 1.8bb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using %AP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
80 a 111 c 122 g 40 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 353)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG386035 353 bp mRNA EST 12-MAR-2001
602455204F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4583473 5',
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Will Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1307 row: h column: 02
Plate: LLCM1307 row: h column: 02
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: ATCC
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DEFINITION

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ó DЪ ORGANISM

AUTHORS

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Tuncord Cene Index

Unpublished (1947)

Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Famert Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento

Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The

1.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:

info@image.lnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: A.K. Winteroe
Contact: A.K. Winteroe
Department of Animal Science and Animal Health, Division of Animal
Genetics, The Royal Veterinary and Agricultural University
Bulowsvej 13, 1870 Frederiksberg C, Denmark.
Location/Qualifiers
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             F14893 355 bp mRNA EST 09-SEP-1996
SSC1D08 Porcine small intestine cDNA library Sus scrofa CDNA clone
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 388)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL CARP http://www.ncbi.nlm.nih.gov/ncicgap.
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Wintero,A.K., Fredholm,M. and Davies,W.
Evaluation and characterization of a porcine small intestine CDNA library: analysis of 839 clones
Mamm. Genome 7 (7), 509-517 (1996)
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; CetarLiodactyla; Suina; Suidae; Sus.
       09-SEP-1996
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/organism="Sus scrofa"
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/clone=lib="Porcine small intestine cDNA llbrary"
/note="directionally cloned cDNA in XLI-blue MRF'"
/note="directionally cloned cDNA in XLI-blue MRF'"
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                                                                  c1d08, mRNA sequence.
F14893
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMI-BT0742-020 500-211-e08&t3*2000-05-02&t4=1)
Seq primer: puc 18 forward High quality sequence start: 16 High quality sequence start: 16 High quality sequence Stop: 354.
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//dev_stage="Addit"
//note="Organ: breast: Vector: puc18; Site_1: Smal: Site_2:
Smal: A mini-library was made by cloning products derived
from ORESTES PER (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 354)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. aud Simpson,A.J.
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CM1-BT0742-020500-211-e08 BT0742 Homo sapiens CDNA, mRNA sequence.
BE092997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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  Score 14; DB 11;
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/db_xref="taxon:9606"
/clone_lib="BT0742"
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     100.0%; 5
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Fax: +55-11-2707001
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Best Local Similarity 100.

Matches 14: Conservative
       Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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FEATURES

BASE COUNT ORIGIN

13

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Gaps

us-09-904-420a-5.rst

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Email: h-lewinguiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AC 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Ouality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
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Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine ESTs
Unpublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW463205 405 bp mRNA EST 24-FEB-2000 BP230012A10B5 Soares normalized bovine placenta Bos taurus cDNA clone BP230012A10B5 5', mRNA sequence.
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BACKWARD: ATTAACCCTACACTAAAG
Insert Length: 405 Std Error: 0.00
Plate: BP230012A10 row: B column: 5
Seq primer: ACCGATAAAAATTACACACAGA
High quality sequence stop: 405.
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Fax: 217 244 5617
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/sex="female"
/lab_host="DH10B"
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**M.B. (1996), Genome Research 6(9): 791-806."
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Consensus quality: 17721 bases at least 020
Consensus quality: 17721 bases at least 020
Consensus quality: 17740 bases at least 020
Estimated insert size: 182000; agarose-fp estimation
Ouality coverage: 8.8 in 020 bases; agarose-fp estimation
Ouality coverage: 8.91 in 020 bases; sum-of-contigs estimation
VOTE: This is a 'working draft' sequence. It currently
consists of 21 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

10083; gap of unknown length
10084; 24409
24509; agap of unknown length
24509
36979; contig of 12370 bp in length
24509
36979; contig of 1335 bp in length
44544
47523; contig of 3775 bp in length
47524
47623; gap of unknown length
47524
47623; gap of unknown length
53214
53313; gap of unknown length
53214
53213; contig of 550 bp in length
53214
53213; contig of 550 bp in length
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53213; contig of 1800 bp in length
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53213; contig of 1800 bp in length
53214
53213; contig of 1800 bp in length
58877; contig of 1800 bp in length
58878; contig of 1800 bp in length
58879; contig of 1800 bp in length
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of 15122 bp in length
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of 2419 bp in length
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/db_xref="taxon:10090"
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Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 Lis sequence version replaced 91:8810357.
-----Genome Center
Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC073740 186243 bp DNA HTG 18-JUL-2000
Mus musculus clone RP23-274122, WORKING DKAFT SEQUENCE, 11 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Summary Statistics
Consensus quality: 15548 bases at least 040
Consensus quality: 18263 bases at least 030
Consensus quality: 184188 bases at least 030
Consensus quality: 184188 bases at least 030
Estimated insert size: 202290; agarose fp estimation
Estimated insert size: 185793; agarose fp estimation
Quality coverage: 6.58 in 020 bases; agarose-fp estimation
Quality coverage: 7.17 in 020 bases; sum-of-contigs estimation
**NOTE: This is a "working draft's sequence. It currently
** consists of 11 contigs. Gaps between the contigs

** are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * is believed to be correct as given, however the pieces of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 438 contig of 438 bp in length

* 539 12616 contig of 12078 bp in length

* 12617 12716 gap of unknown length

* 24950 25049; gap of unknown length

* 24950 25049; gap of unknown length

* 25550 42617; contig of 1258 bp in length

* 25550 contig of 1858 bp in length

* 26560 gap of unknown length

* 2717 gap of unknown length

* 28551 gab of unknown length
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                               ;
                                                                                                                                                                              Length 179641;
                          /clone_lib="RPCI mouse BAC library 23"
44967 a 46477 c 44480 g 41715 t 2002 others
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                               ;
                                                                                                                                                                              Score 17; DB 2;
Pred. No. 62;
                                                                                                                                                                                                                                               Mismatches
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Center clone name: RPCI-23_274122
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/clone="RP23-159B10"
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AC073740.2 GI:9256778
HTG; HTGS_PHASE2; HTGS_DRAFT.
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2 (bases 1 to 186243)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                              Db 156342 CATGCATTACCCACCA 156358
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/product="T cell factor l splice form D"
/protein_id="CAA87439.1"
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/translation="MYKER12"
/translation="MYKER12"
/translation="MYKER12"
/translation="MYKER12"
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/translation="MYKER12"
/translation="MYKER1419"
/translation="MYKER14
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Buckaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1165)
Mayer,K., Wolff,E., Clevers,H. and Ballhausen,W.G.
The human high mobility group (HMG)-box transcription factor TCF-1:
novel isoforms due to alternative splicing and usage of a new exon
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Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachantage 10, Erlangen, Germany, D-91054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSTCFIE 1165 bp mRNA PRI 09-JAN-1995
H.sapiens TCF-1 mRNA for T cell factor 1 splice form E.
Z47362
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Inch human T cell transcription factor-1 gene. Structure, localization, and promoter characterization
J. Biol. Chem. 267 (12), 8530-8536 (1992)
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                                                                                                                        <u>"</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="alternative ORF specific for TCF-1D"
407 c 265 g 171 t
                                                                                                                    /standard_name="T cell factor 1 splice form
/citation=[1]
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.1%; Score 16; DB 9; Length 111
100.0%; Pred. No. 7e+02;
ive 0; Mismatches 0; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="lymphoma"
/cell_type="T-lymophocyte"
/cell_line="Jurkat"
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1. .1115
/gene="TCF-1"
2. .754
                                                                                          /gene="TCF-1"
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Ballhausen, W.G.
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hes 16; Conservative
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butaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1115)
Mayer,K., Wolff,E., Clevers,H. and Ballhausen,W.G.
The human high mobility group (HMG)-box transcription factor TCF-1:
novel isoforms due to alternative splicting and usage of a new exon
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Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
Location/Qualifiers
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H.sapiens TCF-1 mRNA for T cell factor 1 splice form D.
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van de Wetering, M., Oosterwegel, M., Holstege, F., Dooyes, D.,
Suljkerbuijk, R., Geurts van Kessel, A. and Clevers, H.
The human T cell transcription factor-1 gene. Structure,
Jenol Chem. 267 (12), 8530-8536 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 17; DB 2; Length 186243; 100.0%; Pred. No. 62; 0; Mismatches 0; Indels 0;
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      2651 94922: contig of 2272 bp in length 9523 9522: gap of unknown length 10721 97120: contig of 1998 bp in length 10721 97120: contig of 1998 bp in length 17121 157072: contig of 59952 bp in length 1073 157172: gap of unknown length 17172: gap of unknown length 17172: gap of unknown length 171863 174962: gap of unknown length 1963 17840: contig of 3478 bp in length 1963 17840: contig of 3478 bp in length 1863 17840: contig of 7703 bp in length 186243: contig of 7703 bp in length 1963 186243
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="Taxon:10090"
/clone="Rp23-274122"
/clone_lib="RPCI mouse BAC library 23"
/ 47751 c 48436 g 45300 t 1001 others
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/db.xref="taxon:9606"
/tissue_type="lymphoma"
/cell_type="T-lymophocyte"
/cell_line="Jurkat"
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Ballhausen, W.G.
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Matches 17; Conservative
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HSTCF1D
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us-09-904-420a-4.rge

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/codon_start=1
/codon_start=1
/product==r cell factor 1, splice form A"
/product==r cell factor 1, splice form A"
/product==r cell:36786"
/db_xref="G1:36786"
/db_xref
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/translation="MYKETVYSAFNLLMHYPPPSGAGOHPOPPLHKANOPPHGVPO
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2014)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van de Wetering,M.
Direct Submission
Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical
Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,
The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 EC 2814)
van de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H.
Identification and cloning of TCF-1, a T lymphocyte-specific
transcription factor containing a sequence-specific HMG box
ENBO J. 10 (1), 123-132 (1991)
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Human TCF-1 mRNA for T cell factor 1 (splice form B).
X59870 X5529
X59870.1 GI:36787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 1254;
6.8e+02;
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/db_xref="taxon:9606"
/cell_type="T lymphocyte"
/cell_line="Jurkat and HPB-ALL"
/clone_lib="cDNA"
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/db_xref="GI:36788"
                                                                                                                                                                                                                                                                                                                                                                  /gene="TCF-1"
/gene="TCF-1"
/note="alternative splice site"
/note="alternative splice site"
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/gene="TCF-1"
/note="HMG box"
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Matches 16; Conserv
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                                                                                                                                                                                                                            /product="T cell factor 1 splice form E"
//protein_id="CA847440.1"
//db_xref="C1: 6]9884"
//db_xref="C1: 6]9884"
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LIMIGSGYPGHPAA.PPPSGKOBLQPPEDRNLKTOAESKAEKERFTRPPS
LIMIGSGYPGHPAA.PPPSGARCKARRENGETHPOSCPRKRYTRKPLNA
PMLYMKEMRAKVIAECTLKESAAINOILGRRWHALSREEGOAKYYELARKERCHMQLY
LEGERROPSPYPSDDSALGCPGSPAPQDSPSYHLLPRFPTELLTSPRERHLHPQVSPL
LSASOPOGPHRPPAAPCRAHRYSNRNLRDRWPSRHRTPGRLOEPTP"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,
The Netherlands
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van de Wetering,M., Oosterwegel,M., Dooijes,D. and Clevers,H.
Identification and cloning of TCF-1, a T lymphocyte-specific
transcription factor containing a sequence-specific HMG box
BMBO J. 10 (1), 123-132 (1991)
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Mman TCF1 mRNA for T cell factor 1 (splice form A).
X59869 X55327
X59869.1 GI:36785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="alternative ORF specific for TCF-1E"
422 c 286 g 178 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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Pred. No. 6.9e+02;
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/db_xref="taxon:9606"
/cell_type="T lymphocyte"
/cell_line="Jurkat"
/clone_lib="cDNA"
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                 'evidence=experimental
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1. .1254
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100.0%; Pred
0; N
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80. .889
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/gene="TCF-1"
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nes 16; Conserv
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FMLYMKEMRAKVIAECTIKESAAINQILGRRWHALSREEQAKYYELAEKERQLHMQLY
PGWSARDNYCKKRRSREKHQESTTETNWPRELKDGNGQESLSMSSSSSPA"
join(829...924,970...1074,1120...1209,1255...1374,1420...1581,
1691...1798,1843...1890,2054...2134)
925...970
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Catarrhini, Hominidae, Homo.
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Human TCF-1 mRNA for T cell factor 1 (splice form C).
X59871, X53289
X59871.1 G1:36789
UNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
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Pred. No. 5.5e+02;
0; Mismatches 0;
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Eukaryota; Metazoa; Chordala;
Mammalia; Eutheria; Primates;
Ja (bases 1 to 2910)
van de Wetering,M.
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100.0%; Pic
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/gene="TCF-1"
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/gene="TCF-1"
                                                                                                                                  970. .1074
/gene="TCF-1"
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/gene="TCF-1"
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/gene="TCF-1"
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/gene~"TCF-1"
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/number=6
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1210. .1254
/number=3
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/number=4
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929 c
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/number=1
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1799. .184
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Matches 16; Conservative
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1691. .1798,1843. .1890,2054. .2134)
/gene="TCF-1"
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/db_xref="G1:6006565"
/db_xref="G1:6006565"
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LMLGSGVPGHPAAIPHPAIVPPSGKQELQPFDRNLKTQAESKAEKEAKKPTIKKPLNA
             LSLYEHFNSPHPTPAPADISOKOVHRPLQTPDLSGFYSLTSGSMGQLPHTVSWFTHPS
LMLGSGVPGHPAAIPHPAIVPPSGKOELQPFDRNLKTQAESKAEKEAKKPTIKKPLNA
FMLYNKEMRAKVIAECTLKESAAINQILGRRWHALSRREGOAKYYELARKERQLHMQLY
PGWSARDNYGKKRRSREKHQESTTGGKRNAFGTYPEKAAAPAPFLPMTVL"
539. .769
/gene"TCF-1"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2855)

Van de Wetering, M., Oosterwegel, M., Holstage, F., Dooyes, D.,

Suijkerbuijk, R., Geurts van Kessel, A. and Clevers, H.

The human T cell transcription factor-1 gene. Structure,

1 coalization, and promoter characterization

3 Biol. Chem. 267 (12), 8530-8536 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2855)
Van de Wetering,M., Castrop,J., Korinek,V. and Clevers,H.
Extensive alternative splicing and dual promoter usage generate
Tcf-1 protein isoforms with differential transcription control
                                                                                                                                                                                                                                                                                                Gaps
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Van de Wetering, M.L.
Direct Submission
Submitted (07-JAN-1992) M.L. Van De Wetering, Department of Immunology, P.O. Box 8550, 3508 GA Utrecht, THE NETHERLANDS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                             Score 16; DB 9; Length 2814;
Pred. No. 5.5e+02;
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T-cell transcription factor; transcription factor.
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831 c 648 g 572 t
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Mol. Cell. Biol. 16 (3), 745-752 (1996)
96182076
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/clone="phi-TCF-[5,8,11]"
/map="5q31.1"
829. 924

    2855
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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Homo sapiens TCF-1 gene.
X63901
                                                                                                           /note="HMG box"
810
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                                                                                                                                                      /gene="TCF-1"
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1 (bases 1 to 84544)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 5

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC009012 84544 bp DNA HTG 19-APR-2001 Homo sapiens chromosome 5 clone XXpl-360D11, WORKING DRAFT SEQUENCE, 7 ordered pieces.
transcription factor containing a sequence-specific HMG box EMBO J. 10 (1), 123-132 (1991) 91114695
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                                                                                                                                                                                                                                                           /product="T_cell factor 1, splice form C"
Protein_lad=CRA4528.1"
/db_xref="GI:36790"
/db_xref="SWISS-PROT:P36402"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC009012.3 GI:12830104
HTG; HTGS_PHASE2; HTGS_DRAFT: HTGS_ACTIVEFIN.
                                            Location/Qualifiers
1. 2910
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T lymphocyte"
/cell_ine="Jurkat and HPB-ALL"
/clone_lib="CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                810
/gene="TCF-1"
/note="alternative splice site"
a.c.n c 671 g 597 t
                                                                                                                                                                                 /evidence=experimental
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                              /note="HMG box"
                                            See also X59869-X59871.
                                                                                                                                                                                                        /gene="TCF-1"
80. .886
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                                                                                                                                                                                                                                  /gene="TCF-1"
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/gene="TCF-1"
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Consensus quality: 78189 bases at least Q40
Consensus quality: 82001 bases at least Q30
Consensus quality: 8201 bases at least Q30
Consensus quality: 9201 bases: pulse field gel estimation
Duality coverage: 6.34 in Q20 bases: pulse field gel estimation
Quality coverage: 6.34 in Q20 bases: pulse field gel estimation
Quality coverage: 6.74 in Q20 bases: pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 2990 3079: gap of unknown length
* 34577 34576: contig of 24586 bp in length
* 59263 59362: gap of unknown length
* 59263 59362: gap of unknown length
* 76011 76110: gap of unknown length
* 76011 76110: gap of unknown length
* 76011 7613: contig of 16648 bp in length
* 76111 79613: contig of 1868 bp in length
* 76111 79613: contig of 1868 bp in length
* 76111 79613: contig of 18795 bp in length
* 76111 79613: contig of 18795 bp in length
* 80650 80749: gap of unknown length
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5 clone CTC-250113, WORKING DRAFT SEQUENCE,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 86914)
DOE Joint Genome Institute.
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN
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    .84544
/organism*"Homo sapiens"
/db_xref="taxon:9606"

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Unpublished
2 (bases 1 to 86914)
DOE Joint Genome Institute.
Direct Submission
                    Center Project Name: 1189075, H71
Center clone name: XXp1-360D11
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lordered pieces.
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110943
111043
127291
127391
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Consensus quality: 85602 bases at least Q30
Consensus quality: 86302 bases at least Q30
Consensus quality: 86312 bases at least Q20
Estimated insert size: 86914; sum-of-contigs estimation
Estimated insert size: 86914; sum-of-contigs estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation
Quality coverage: 6.56 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
consists of locontigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 86914: contigs G 86914 bp in length.
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Submitted (03-A00-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
on Apr 20, 2001 this sequence version replaced gi:11178048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC009017 159420 bp DNA HTG 20-APR-2001
Homo sapiens chromosome 5 clone XXpl-929G6, WORKING DRAFT SEQUENCE,
26 unordered pieces.
Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7710593.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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Center clone name: CIT-HSPC_250113
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                 Web site: http://www.jgi.doe.gov
                                                                                       ------Genome Center
Center: Joint Genome Institute
Center Code: JGI
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2 (bases 1 to 159420)
DOE Joint Genome Institute.
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Consensus quality: 142845 bases at least 040
Consensus quality: 150910 bases at least 030
Consensus quality: 152756 bases at least 030
Consensus quality: 152756 bases at least 020
Estimated insert size: 80000; pulse field gel estimation
Estimated insert size: 156920; sum-of-contigs estimation
Quality coverage: 8.41 in 020 bases; pulse field gel estimation
Quality coverage: 4.29 in 020 bases; sum-of-contigs estimation
* NOTE: This is a "working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* in this sequence record is
                                                                                                                                                                                                                                                                                                                                       * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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gap of unknown length
contig of 1543 bp in length
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Center: Joint Genome Institute
                                                                       Project Information
Center Project Name: 1189133,
                                                                                                           Center clone name: XXp1-929G6
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Submitted (14-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: hunguery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Jan 23, 2001 this sequence version replaced gi:6249356.

During sequence assembly data is compared from overlapping clones,
where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL: Sw. SMISSPROT: Tr:, TREMBL: WP:, WORMPEP: Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
RAPI-269MIS is from the library RPCI-1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HS269M15 177562 bp DNA PRI 20-JUN-2001 Human DNA sequence from clone RPI-269M15 on chromosome 20q12-13.12 Contains a gene similar to peptidylprolyl isomerase (cyclophilin), and the 5' end of the PTPRT gene encoding protein tyrosine phosphatase, receptor type, T, ESTs, STSs, GSSs and CpG Islands, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                          Length 159420;
                                                                                                                                                                                               2506 others
     143781: gap of unknown length
159420: contig of 15639 bp in length.
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                                                                                                                                                                /clone="XXp1-929G6"
38414 c 39218 g 39915 t
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                                                                        1. .159420
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                      Location/Qualifiers
1. .159420
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100.0%; Pre-
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HTG; CpG Island; PTPRT.
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Best Local Similarity
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KEYWORDS
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TITLE
JOURNAL
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/note="AluJ/FRAM repeat: matches 226, .278 of consensus" 6018. .6069
/note="AluJ/FRAM repeat: matches 226. .278 of consensus" 6133 .6167
/note="Alu repeat: matches 76. .110 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5410. 5469
//note="AluJ/FRAM repeat: matches 215. 278 of consensus" 5469. 5519
//note="AluJ/FRAM repeat: matches 227. 278 of consensus" 5518 . 5569
//note="AluJ/FRAM repeat: matches 226. 278 of consensus" 5568 . 5619
//note="AluJ/FRAM repeat: matches 226. 278 of consensus" 5688 . 5619
//note="AluJ/FRAM repeat: matches 226. 278 of consensus" 5618 . 5669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .278 of consensus"
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/note="L2 repeat: matches 2619. .2750 of consensus"
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forter Alusp repeat: matches 55. .303 of consensus"
complement(3322. .3994)
/note="match: GSS: Em:AQ014397"
                                                                                                                                                                                                                                                                                                                                     2215. .2334 Consensus
/note="MER81 repeat: matches 1. .114 of consensus"
2408. .2041
                                                                                                                                                                                                                                                     .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                      /note="MifflE repeat: matches 1. .51 of consensus" 9677. .10127
                                                                                                                                  407. .593 ....matches 20. .221 of consensus" /note="MIR repeat: matches 20. .214 of consensus" 1081. .1205
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/note="MIR repeat: matches 3. .126 of consensus"
5269. 5319
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10185. 10222
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/note="l/R833 repeat: matches 312.
2215. .2334
                                                                                                                                                                                                                                    1407. .1593
/note="MER5A repeat: matches 1.
                                                                                                                                                                                                                                                                    complement(1544 .1966)
/note="match: GSS: Em:AQ880374"
1783. .1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5818. .5869
/note="AluJ/FKAM repeat: ma
/5868. .5919
/note="AluJ/FKAM repeat: ma
/5918. .5969
/note="AluJ/FKAM repeat: ma
/5968. .6019
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/note="AluJ/FRAM repeat: m2568. 5819

/note="AluJ/FRAM repeat: m2568. 5819
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/note="AluJ/FRAM repeat:
5369. .5419
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5668. .5719
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                        /map="q12-13.12"
/clone="RP1-269M15"
                                                                                          /clone_lib="RPCI-1"
15. .221
                                         /chromosome="20"
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.118 of consensus"

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Consensus quality: 174733 bases at least 040
Consensus quality: 186693 bases at least 030
Consensus quality: 196547 bases at least 030
Consensus quality: 196547 bases at least 020
Estimated insert size: 165000; pulses field gel estimation
Betimated insert size: 165000; pulses field gel estimation
Cuality coverage: 7.77 in 020 bases; sum-of-contigs estimation
Quality coverage: 6.47 in 020 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                             DNA HTG 20-APR-2001
5 clone CTB-113120, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced 91:7708985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euleleostomi;
Catarrhini; Hominidae; Homo.
23388. .23477
/note="MBER8A repeat: matches 29. .118 of consens
23481. .23505
/note="MER3 repeat: matches 1. .25 of consensus"
                                                                                                  Length 177562;
                                                                                       DB 9; Leng...
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gap of unknown l
contig of 1322 b
gap of unknown l
contig of 1078 b
gap of unknown l
contig of 1024 b
gap of unknown l
gap of unknown l
contig of 1024 b
                                                                                                                         ilarity 100.0%; Pred. No. 2e+
Conservative 0; Mismatches
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Center Project Name: 107808, H233
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Web site: http://www.jgi.doe.gov
                                                                                                    Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing of Human Chromosome
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Eukaryota; Metazoa; Chordata;
Marmalia; Eutheria; Primates;
1 (bases 1 to 20083)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
2 (bases 1 to 200831)
DOE Joint Genome Institute.
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Homo sapiens chromosome
29 unordered pieces.
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1215:
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2667:
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                           /note="Wir repeat: matches 22. .153 of consensus"
13311. .13899
/note="LIMBB repeat: matches 5536. .6145 of consensus"
14184. .14475
/note="AluSc repeat: matches 1. .289 of consensus"
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12169. 12469
/note="Alusx repeat: matches 1. .299 of consensus"
12612. 12641
                          /note="%1usq repeat: matches 1. .293 of consensus" 10602. .10640 //note="WirzCA repeat: matches 459. .497 of consensus" 10629. .11083 //note="WirIt repeat: matches 9. .504 of consensus" 11517. .11716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Continues in dJ914M10 (Em:AL121763)
the full gene is contained in the following clones
Em:AL121763, Em:AL021395, Em:AL031656, Em:AL022239,
Em:293942, Em:AL024473 and Em:AL035459, Em:AL049812,
Em:AL136461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MASLAALALSLILRLOLPPLPGARAOSAA"
19684. 19729
/note="123 copies 2 mer gg 73% conserved"
19747. 19794
/note="16 copies 3 mer cgc 85% conserved"
20884. 20941
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23220. .23359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/evidence=not_experimental
/product="dJ269M15.2 (Protein tyrosine phosphatase,
receptor type, T (PRTPRHO, KIAA0283))"
/protein_id="CAC24740.2"
/db_xref="GI:14530721"
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7. 21324 repeat: matches 2673. .2742 of consensus"
21633. .22115
7. 7. 22115 m:AQ063598"
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//note="Liz repeat: matches 2298. .2490 of consensus"
22558. .22605
//note="MIR repeat: matches 81. .135 of consensus"
22715. .22845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="dJ269M15.2 (Protein tyrosine phosphatase,
receptor type, T (RPTPRHO, KIAA0283))"
/evidence=not_experimental
complement(19423..19746)
                                                                                                                                                                                                                                                                                                                                                                                                   note="Alusx repeat: matches 5. .306 of consensus"
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/note="MER3 repeat: matches 1. .152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
19006. 19030
/note="Single clone region. Assembly confirmed by
restriction enzyme digest data."
complement(<19423. 19746)
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 20. .241 of consensus" complement(16131. .16704)
                                                                                                                                                                                                                                    note="15 copies 2 mer aa 86% conserved"
13155. 13285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="match: GSS: Em:AQ376253"
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match: proteins: Tr:O43655"
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/gene="PTPRT"
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/note="CpG island"
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E l (bases 1 to 216)

E Deloukas, P., Buck, D., Langford, C., Ross, M.T. and Hunt, S.E.

Direct Submission

L Submitted (17-APR-1997) The Sanger Centre, Wellcome Trust Genome

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
hunquery@sanger.ac.uk

Vector: pBS15SF7 | Primer A : TCATGCATTACCCACCAGA; Primer B :
AAGGAATGGAAAGAGGAGAAGG; amplimer size : 145 bp) was mapped to
chromosome 20 using Radiation Hybrid panel Genebridge 4 (GB4).
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/db_xref="G1:6165634"
/translation="MNYARFITAASAARNESPIRTWTDILSRGPKSMISLAGGLPNPN
MFPFRTAVITYENGRYTOFGBEMMKRALQYSPSAGIPELLSWLKOLGIKLHNPPTIHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gatti,S., Breton,J., Mostardini,M., Mosca,M., Tarroni,P., Schwarcz,R., Speciale,C., Okuno,E., Toma,S. and Benatti,L. Cloning of human L-kynurenine/alpha-aminoadipate aminotransferase
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2046)
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Gattl, S., Breton, J., Mostardini, M., Mosca, M., Tarroni, P.,
Schwarcz, R., Speciale, C., Okuno, E., Toma, S. and Benatli, L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.4; DB 11; Length 216; pred. No. 2.1e+03; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="EBV lymphoblastoid cell line"
/clone_lib="SC2OpF"
/clone="SC2OpF15G5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="1,-kynurenine/alpha-aminoadipate
aminotransferase"
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Pasteur, 10, Nerviano, Milano 20014, Italy
location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
454. .1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome-"20"
                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
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94.18;
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H.sapiens flow sorted chromosome 20 HindIII fragment, SC20pF15G5,
Sequence tagged site.
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/db_xref="taxon:9606"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Partial cDNA encod	Probe #8447 used t	cDNA encoding a hu	Human polynucleoti	Human cDNA sequenc	Human polynucleoti	Breast cancer tumo	DNA molecule encod	Human breast tumou	Drosophila melanog	HGV sequence ampli	
SUMMARIES	1		AAZ46032	AA139761	AAZ46023	AAI59213	AAH18256	AAI59251	AAX83386	AAV68924	AAC80909	AAH29229	AAV66258	
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	Query Match Length DR		243	290	2125	2348	2184	2737	289	289	289	378	401	
d	Query		9.06	90.6	90.6	90.6	88.2	88.2	84.7	84.7	84.7	84.7	84.7	
	Score		15.4	15.4	15.4	15.4	15	15	14.4	14.4	14.4	14.4	14.4	
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WO200000594-A2 Homo sapiens

06-JAN-2000.

sednence	sednence am	variant 7244	HGV variant K27 DN	HGV variant K30 DN	Polynucleotide seq		leotide se	3	34 Seq ID	34 Seq ID	S		Hepatitis G virus	HGV sequence ampli	HGV variant T56957	otid	Se	Hepatitis G virus	Schizochytrium sp.	M. alpina desatura	Partial DNA sequen	Schizochytrium sp.	ing		Hepatitis GB virus	Human cerebellin-2	z	HGJ177		u	HGJ191	Fragment F1029 of	Fragment HGJ1789 o
AAV66259	AAV66260	AAV56221	AAV56222	AAV56223	AAX16533	AAX16534	AAX16535	AAX02496	AAX02497	AAX02498	AAV82276	AAV82277	AAV82278	AAV66247	AAV56210	AAX16522	AAX02485	AAV82265	AAV63636	AAX00914	AAV82635	AAA09446	AAA14587	AAT96420	AAT96405	AAZ11192	AAS21286	AAV23082	AAV23075	AAV23080	AAV23079	AAV23084	AAV23078
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ALIGNMENTS

AA246032 standard; cDNA; 243 BP

AAZ46032

RESULT

AAZ46032;

Transferase; HUTRAN-2; kynurenine/alpha-aminoadipate aminotransferase; autoimmune disorder; inflammatory disorder; AIDS; atherosclerosis; adult respiratory distress syndrome; allergy; asthma; trauma; autoimmune thyroiditis; bronchitis; Crohn's disease; diabetcs mellitus; gout; Grave's disease; osteoarthritis; osteoporosis; pancrealis; psoriasis; rhemmatoid arthritis; infection; neurological disorder; picks disease; Huntingdon's disease; extrapyramidal disorder; viral central nervous system disease; prion disease; central nervous system disorder; peripheral nervous system disorder; peripheral nervous system disorder; peripheral nervous system disorder; and disorder; mental disorder; schizophrenic; anxietis; contral disorder; mental disorder; schizophrenic; anxietis; contral disorder; dyspepsia; anxietis; contral disorder; dyspepsia; Partial cDNA encoding a transferase designated HUTRAN-2 fragment. indigestion; gastritis; anorexia; nausea; abdominal angina; gastroenteritis; intestinal obstruction; peptic ulcer; irritable bowel syndrome; diarrhoea; constipation; gastrointestinal haemorrhage; cancer; ss. (first entry) 25-APR-2000 Chen W, Rank DR;

us-09-904-420a-4.rng

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Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                    analyzing gene expression in human placenta
                                                                                                                                                                                                              Claim 25; SEQ ID No 8447; 654pp; English.
                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
          2000US-0632366.
2000US-0632366.
2000US-0234687.
           30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0532866.
27-SEP-2000; 2000US-0236889.
04-OCT-2000; 2000US-0336359.
2000US-0207456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                  Novel human transferases used for the diagnosis, treatment, and prevention of autoimmune/inflammatory, neurological, reproductive and gastrointestinal disorders and cancer
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                                                                                   Corley NC;
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                                                                                                                                                                                                         Disclosure; Page 86; 95pp; English.
                                                                                     Bandman O, Hillman JL,
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94.1%;
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ID AA139761 standard; DNA; 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312.
                                  98US-0109204.
       99WO-US14651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 catccattacccaccca 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 catgcattacccaccca 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                            (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                           WPI; 2000-147267/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157272-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-2001
       29-JUN-1999;
                                 30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                   Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA139761;
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Transferase; HUTRAN-2; kynurenine/alpha-aminoadipate aminotransferase;

W autoimmune disorder; inflammatory disorder; AIDS; atherosclerosis;

W autoimmune thyroiditis; bronchilis; Crohn's disease; diabetes mellitus;

W autoimmune thyroiditis; bronchilis; Crohn's disease; diabetes mellitus;

W poriasis; rheumatoid arthritis; infection; neurological disorder;

W priox disease; stematoid arthritis; infection; neurological disorder;

W picks disease; Huntingdon's disease; dementia: Parkinson's disease;

W priox disease; central nervous system developmental disorder;

W priox disease; central nervous system disorder;

W priox disease; central nervous system disorder;

W priox disease; central nervous system disorder;

W anxiety; reproductive disorder; dastrointestinal disorder; disorder;

W pastroenteritis; intestinal obstruction; peptic ulcer;

W dastroenteritis; intestinal obstruction; peptic ulcer;

W dastrointestinal haemorrhage; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
The present invention relates to single exon nucleic \mathscr{A}cid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding a human transferase designated HUTRAN-2.
                                                                                                                                                                                                                                                     Sequence 590 BP; 198 A; 99 C; 149 G; 144 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                    90.6%; Score 15.4; 1
94.1%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ46023 standard; cDNA; 2125 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 catgcattacccaccca 17
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 94.1
Matches 16; Conservative
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Wang J, Wang Z, 1
Zhao QA, Zhou P,
                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                          Wang Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.N.S disorders.
            WO200153312-A1.
                                                                                                                                             25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification
                                                                                                                                                                                                                                          19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                             21-JAN-2000;
                                                  26-JUL-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH18256;
                                                                                                                                                                                                                                                                                                                                          rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH18256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a transferase polypeptide, designated HUTRAN-2. The HUTRAN cDNA sequence is derived from Incyte clone 2150892. The sequence is obtained from the partial sequences AA246032-38. The polypeptide is a kynurenine/alpha-aminoadipate aminotransferase. The HUTRAN polypeptides, polynucleotides, agonists, antagonists, and antibodies can be used to diagnose, treat or prevent autoimmune/ inflammatory disease (e.g. ADDS, adult respiratory distress syndrome, allergies, asthma, atherosclerosis, autoimmune thyroiditis, bronchitis, crohn's disease, diabetes mellitus, gout, Grave's disease, osteoarthritis, osteoporosis, pancreatis, psoriasis, rheumatoid arthritis, infections, trauma, neurological disorders (e.g. epilepsy, ischemic cerebrovascular disease, stroke, Alzheimer's disease, picks disease, Huntingdon's disease, dementia, parkinson's disease, prion diseases, central nervous system developmental disorders, prion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders, muscular dystrophy, neuromuscular disorders, peripheral nervous system disorders, mental disorders, schizophrenic, anxiety, reproductive disorders and gastrointestinal disorders (e.g. dyspepsia,
                                                                                                                                                                                                                                                                   Novel human transferases used for the diagnosis, treatment, and prevention of autoimmune/inflammatory, neurological, reproductive and gastrointestinal disorders and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            indigestion, gastritis, anorexia, nausea, abdominal angina, asstroenteritis, intestinal obstruction, intestinal tract infections, peptic ulcer, irritable bowel syndrome, diarrhoea, constipation, gastrointestinal haemorrhage, and cancer.
                                                                                                                                                     corley NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                     Guegler KJ, Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI59213 standard; cDNA; 2348 BP.
                                                                                                                                                     Bandman O, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 81; 95pp; English.
                                        99WO-US14651.
                                                                            98US-0109204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 446 catccattacccaccca 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 catgcattacccaccca 17
                                                                                                                   (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                              WPI; 2000-147267/13.
P-PSDB; AAY54592.
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                                        29-JUN-1999;
                                                                          30-JUN-1998;
                                                                                                                                                                            Patterson C;
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  06-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity such as Immune system suppression, Activity, Chemotactic/chemokinetic activity, haemostatic and thrombolyric activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                      ά
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                                                                                                                                                                                                                                                                                                                                                                                      Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \dot{\ }
                                                                                                                                                                                                                                                                                                                                                                                      Ren F, Wi
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
                                                                                                                                                                                                                                                                                                                                                                               Chen R, Ma Y, Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.4; DB
Pred. No. 46;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ 1D NO 1416; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA sequence SEQ ID NO:18214.
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                                                  2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
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Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                2000US-0727344.
26-DEC-2000; 2000WO-US34263.
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us-09-904-420a-4.rng

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RESULT
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The present invention describes primer sets for synthesising 5602

(a) an oligo-dr primer and an oligonucleotide complementary

comprises: (a) an oligo-dr primer and an oligonucleotide complementary

to the complementary strand of a polynucleotide which comprises one of

the 5602 nucleotide sequences defined in the specification, where the

oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises a 3'-end sequence, where the

coligonucleotide comprises at least 15 nucleotides and the combination of

the 5'-end sequences'3'-end sequence is selected from those defined in

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primers are useful for synthesising polynucleotides,

particularly full-length cohAs. The primers are also useful for the

cohAs easily without any specialised methods. AAH03166 to AAH18638 and

AAB95893 represent human amino acid sequences; and AAH18632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS;
                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                              Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 22; Length 2184;
Pred. No. 75;
                                                                                                                                                                            Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2184 BP; 458 A; 635 C; 635 G; 456 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID 18214; 2537pp + CD ROM; English.
                                                                                                                                                                            Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 1454.
                                                                                                                                                                                           Wakamatsu
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100.08; P1.
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                                                                                                                                                                              Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI59251 standard; cDNA; 2737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.28;
                                                                                     27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                 28-JUL-2000; 2000EP-0116126.
                                                                           99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 atgcattacccaccc 16
                                                                                                                                                     (HELI-) HELIX RES INST.
                                                                                                                                                                                           Sugiyama T,
                                                                                                                                                                                                                   WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                              Isoqai T,
                                                                                                                                                                                                                                                                                  full-length cDNAs
 EP1074617-A2.
                                                                          29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-2001
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                                                                                                                                                                              Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with noctropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotinetic; thrombolytic; drug screening; arthritis; inilammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren F, Wa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2737 BP; 484 A; 840 C; 899 G; 514 T; 0 other;
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Xu C, Xue AJ,
R, Drmanac RT;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1454; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V, Che
Wehrman T, Xu
Goodrich R,
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-062191.
19-CCT-2000; 2000US-063344.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-442253/47.
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Wang 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                 WO200153312-A1.
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                                                                                            leukaemia; ss.
                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                     26-JUL-2001
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Claim 4; Page 141; 187pp; English.
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                                                                                                      Claim 1; Page 101; 173pp; English
Smith JM;
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99US-0429755.
2000US-0534825.
                                                                                                                                                                                                                                                                                                           84.78;
93.88;
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                                                                                                                                                                                                                                                                                                                                       Conservative
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Reed SG,
                         WPI; 1998-557473/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-628403/60.
                                                                                                                                                                                                                                                                                                                         Local Similarity
es 15; Conserv
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 Frudakis TN,
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28-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                 Sequences AAX83201-X83285 and AAX83331-X83415 represent novel breast cancer tumour specific clones which are expressed from a genomic region containing a human endogenous retrovirus (AAX83330). Detection of the clone sequences allows determination of the presence of breast cancer in a mammal. Progression of breast cancer can be monitored by detecting the level of clone expression. Polypeptides encoded by the clones can be used in vaccines to inhibit or prevent breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                  cancer-related DNA from retrovirus antigen (s) - useful for
                               tumour; gene expression; genome; diagnosis; manmal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; breast cancer; breast tumour tissue; diagnosis; treatment; vaccine; epitope; endogenous; retroviral element; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA molecule encoding a breast tumour specific polypeptide #116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.4; DB 18; Length 289;
Pred. No. 1.3e+02;
); Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 289 BP; 101 A; 48 C; 67 G; 73 T; 0 other;
                                            human endogenous retrovirus; vaccine; ss.
     Breast cancer tumour specific clone #140.
                                                                                                                                                                                                                                                                                                               diagnosis and treatment of breast cancer
                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 167; 221pp; English.
                                                                                                                                                                                                                                               Smith JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.78;
93.88;
                                                                                                                                                    97WO-US00485.
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96US-0585392.
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97US-0838762.
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Best Local Similarity 93.8
Matches 15, Conservative
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                                                                                                                                                                                                                                               Reed SG,
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                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
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                                Breast cancer;
                                                                                                W09725426-A2.
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                                                                                                                                                                                                                                               Frudakis TN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                        Homo sapiens
                                                                                                                                                  10-JAN-1997;
                                                                                                                                                                                            11-JAN-1996;
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                                                                                                                                                                               20-AUG-1996;
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                                                                                                                          17-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV68924;
                                                                                                                                                                                                                                                                                                     Breast
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The present sequence is given in a specification relating to compositions and methods for the treatment and diagnosis of breast, cancer. Nucleotide sequences that are preferentially expressed in breast tumour tissue, and the polypeptides encoded by such nucleotide sequences, are used in
                                                                                                                                                                                                                                                 AAV68800 to AAV68998 represent nucleotide sequences which encode human breast tumour specific polypeptides. Detection or measurement of human breast tumour specific polypeptides and nucleotide sequences, or the corresponding RNA in a sample, is used for diagnosis and monitoring of breast cancer. Human breast tumour specific polypeptides and nucleotide sequences, and the vectors containing the DNAs, are also useful in vaccines for inhibiting development (for prevention or therapy) of breast cancer. The polypeptides may also be used to raise monoclonal antibodies, used as immunoassay reagents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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New DNA sequences isolated from endogenous human retroviral element - and related vectors, transformed cells, proteins and antibodies, useful for diagnosis, treatment and prevention of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retter MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 289 BP; 101 A; 48 C; 67 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.4; DB 19;
Pred. No. 1.3e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast tumour-specific cDNA SEQ ID NO: 197.
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us-09-904-420a-4.rng

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atgcattacccaccca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus
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Matches
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                                                                                                            RESULT
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compositions and vaccines to inhibit the development of cancer, especially breast cancer. The progression of a cancer may be monitored by carrying out detection of tumour-specific antigens at subsequent time points and comparing the results from the different time points. CD4 and/or CD8+ T-Cells isolated from the cancer patient may be treated with tumour-specific polypeptides, polypurcleotides encoding the polypeptides or antigen presenting cells each of the polypeptides. The cells are then administered to the patient to inhibit development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster. Lack of expression of the protein encoded by this gene leads to a lethal or semi-lethal phenotype. The inventition relates to 902 nucleic acid sequences from genes encoding proteins which are thought to be essential, and to a screening assay for identifying compounds which have a physiological effect on these proteins. Suitable compounds are useful as pesticides and may be used in conjunction with other pesticides and herbicides for crop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is located
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster; fruit fly; essential gene; screening assay; pesticide; crop protection; chromosome 3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is part of an essential gene from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster essential gene fragment, SEQ ID NO: 418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening assays for used for identifying compounds having a physiological effect on proteins identified as being essential
                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                  Score 14.4; DB 21; Length 289;
Pred. No. 1.3e+02;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protection. The gene corresponding to the present sequence
                                                                                                                                                                                Sequence 289 BP; 101 A; 48 C; 67 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 378 BP; 122 A; 77 C; 86 G; 93 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang MY;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAH29229 standard; DNA; 378 BP.
                                                                                                                                                                                                                                      84.7%;
93.8%;
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                           77 ATACATTACCCACCA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIU ) UNIV GLASGOW.
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from different sera by the PCR primers AAM66181-82). The specification describes HGV antigen clones isolated from PNF2161 sera. This sera is obtained from a patient suffering from Non-A Non-B Non-C Non-D Hopatitis Virus, also known as Hepatitis G virus (HGV). HGV antigens can be used in immunoreaction screening for presence of anti-HGV specific antibodies, especially in patient sera, e.g. enzyme linked immunossasy (FLISA). They can also be used as vaccines, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV66231-66 represent the Hepatitis G virus (HGV) sequences, amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide antigens hepatitis G virus - useful as vaccines against the virus and raising antibodies for use in immuno-testing for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                        PNF2161 sera; antigen; immunoreaction screening;
Non-A Non-B Non-C Non-D Non-E Hepatitis virus; HGV;
anti-HGV antibody; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 401 BP; 76 A; 112 C; 137 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            raise the polyclonal and monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 18; Columns 323-324; 206pp; English.
                                                                                                                                                                                                                                                                                           HGV sequence amplified from serum code 7244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wages J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENELABS TECHNOLOGIES INC.
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                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940S-0246985.
940S-0285543.
940S-0285561.
940S-0329729.
940S-0344271.
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                                                                                                                          AAV66258/c
1D AAV66258 standard; DNA; 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0444733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0389886
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393 CATGCATTTCCCACCC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 catgcattacccaccc 16
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nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis G virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1994;
03-AUG-1994;
03-AUG-1994;
26-OCT-1994;
23-NOV-1994;
16-DEC-1994;
15-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-1995;
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RESULT 12 AAV66259/C

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Gaps

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Query Match 84.7%; Score 14.4; DB 22; Length 378; Best Local Similarity 93.8%; Pred. No. 1.4e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0;

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PNF2161 sera; antigen; immunoreaction screening;
Non-A Non-B Non-C Non-D Non-E Hepatitis virus; HGV;
anti-HGV antibody; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGV variant 7244 DNA
                                                                                                                                                                                                                                                                  WPI; 1998-582553/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis G virus.
                                          Hepatitis G virus.
                                                                                                                                                                                                                                              Kim JP,
                                                                                                                           19-MAY-1995;
20-MAY-1994;
03-AUG-1994;
03-AUG-1994;
26-OCT-1994;
                                                                                                        19-MAY-1995;
                                                                                                                                                                               23-NOV-1994;
16-DEC-1994;
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                                                                US5824507-A.
                                                                                    20-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                Fry KE,
                                                                                                                                                                                                                                                                                                            virus
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                           Polypeptide antigens hepatitis G virus – useful as vaccines against the virus and raising antibodies for use in immuno-testing for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 401 BP; 77 A; 112 C; 136 G; 76 T; 0 other;
                                                                                       PNF2161 sera; antigen; immunoreaction screening;
Non-A Non-B Non-C Non-D Non-E Hepatitis virus; HGV;
anti-HGV antibody; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                   Young LM;
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 18; Columns 323-326; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGV sequence amplified from serum code K30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                   HGV sequence amplified from serum code K27.
                                                                                                                                                                                                                                                                                                                                    Wages J,
                                                                                                                                                                                                                                                                                                               (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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      AAV66259 standard; DNA; 401 BP
                                                                                                                                                                                                                95US-0444733.
94US-0246985.
94US-0285543.
94US-028561.
94US-0329729.
94US-034271.
94US-034271.
                                                                                                                                                                                                                                                                                                                                   Linnen JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV66260 standard; DNA; 401
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                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 CATGCATTCCCCACCC 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 catgcattacccaccc 16
                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-582553/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                 Hepatitis G virus.
                                                                                                                                                                                                                           20 MAY - 1994;
03 - AUG - 1994;
03 - AUG - 1994;
26 - OCT - 1994;
23 - NOV - 1994;
16 - DEC - 1994;
                                                                                                                                                                                              19-MAY-1995;
                                                                                                                                                                                                                  19-MAY-1995;
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                                                                                                                                                     US5824507-A.
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                                               23-DEC-1998
                                                                                                                                                                           20-0CT-1998
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                                                                                                                                                                                                                                                                                                                                  Fry KE,
                                                                                                                                                                                                                                                                                                                                                                                                 virus
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AAV66231-66 represent the Hepallitis G virus (HGV) sequences, amplified from different sera by the PCR primers AAV66181-82). The specification describes HGV antigen clones isolated from PNF2161 sera. This sera is obtained from a patient suffering from Non-A Non-B Non-C Non-D Non-E Hepatitis Virus, also known as Hepatitis G virus (HGV). HGV antigens can be used in immunoreaction screening for presence of anti-HGV specific antibodies, especially in patient sera, e.g. enzyme linked immunoassay (ELISA). They can also be used as vaccines, and to raise the polyclonal and monoclonal antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide antigens hepatitis G virus – useful as vaccines against the virus and raising antibodies for use in immuno-testing for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.4; DB 19; Length 401; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 401 BP; 77 A; 109 C; 136 G; 79 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                         Young LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 18; Columns 325-326; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Wages J,
                                                                                                                                                                                                                                                                                                               (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                95US-0444733.
94US-0285543.
94US-0285561.
94US-0329729.
94US-0344271.
94US-034509.
                                                                                                                                                                                                                                                                                                                                                                            Linnen JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 84.7%;
Local Similarity 93.8%;
Les 15; Conservative
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1D AAV56221 standard; DNA; 401
95US-0444733
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Search completed: February 20, 2002, 10:31:56 Job time: 10224 sec
03-AUG-1994;
03-AUG-1994;
03-AUG-1994;
26-OCT-1994;
23-NOV-1994;
15-PEC-1994;
15-PEB-1995;
05-JUN-1995;
                                                                                                                                    Fry KE,
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                                                                                                                                                                                                                                                                                                 This sequence is a used in a method which detects Non-A, Non-B, Non-C, Non-D, Non-E hepatitis G virus (HGV) in a biological fluid sample, e.g. from a test subject, especially using a kit comprising an anti-HGV antibody preparation and a reporter for detecting binding of an HGV polypeptide antigen to the antibody, preferably where the antibody is monoclonal and/or is attached to a solid support and where the reporter is a labelled monoclonal antibody or a labelled competing antigen. The HGV is characterised by producing elevated serum alanine aminotransferase levels in an infected primate, being serologically distinct from hepatitis A, B, C, D and E viruses and having a viral genome containing a nucleic acid region that is selectively hybridisable with a polypeptide having 203 base pairs as given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                          Antibody to hepatitis G virus protein - useful for diagnosis of hepatitis G virus infection
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0
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Non-A, Non-B, Non-C, Non-D, Non-E hepatitis virus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.7%; Score 14.4; DB 19; Length 401; 93.8%; Pred. No. 1.4e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 401 BP; 76 A; 112 C; 137 G; 76 T; 0 other;
                                                                                                                                                                                               Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
                                                                                                                                                                                                                                                                               Disclosure; Column 323-324; 204pp; English
                                                                                                                                                                        (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                      95US-044473.
94US-0246985.
94US-0285543.
94US-0285561.
94US-0329729.
94US-03457509.
95US-03497509.
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ID AAV56222 standard; DNA; 401
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94US-0246985
                 95US-0466033
                                                                                                                                                  95US-0466033
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Matches 15; Conservative
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                                                                                                                                                                                                                      WPI; 1998-361677/31.
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20-MAY-1994;
                 05-JUN-1995;
                                                                                                                                                  05-JUN-1995;
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                                                                                      03-AUG-1994
26-OCT-1994
                                         19-MAY-1995
                                                                            03-AUG-1994
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                                                                                                                         16-DEC-1994
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                                                               03-AUG-1994
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This sequence is a used in a method which detects Non-B, Non-B, Non-C, Non-E hepatitis G virus (HGV) in a biological fluid sample, e.g. from a test subject, especially using a kit comprising an anti-HGV antibody preparation and a reporter for detecting binding of an HGV polypeptide antigen to the antibody, preferably where the antibody is monoclonal and/or is attached to a solid support and where the reporter is a labelled monoclonal antibody or a labelled competing antigen. The HCV is characterised by producing elevated serum alanine aminotransferase levels in an infected primate, being serologically distinct from hepatitis A, B, C, D and E viruses and having a viral genome containing a nucleic acid region that is selectively hybridisable with a polypeptide having 203 base pairs as given in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody to hepatitis G virus protein - useful for diagnosis of hepatitis G virus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 401 BP; 77 A; 112 C; 136 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      Young LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 325-326; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Kim JP, Linnen JM, Wages J,
                                                                                                                                                                                                                                                                                                    (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
94US-0285543.
94US-028558.
94US-028561.
94US-0329729.
94US-0347271.
94US-0357509.
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Best Local Similarity 93.8
Matches 15; Conservative
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Appl Appl Appl Appl

Sequence Sequence Sequence

Sequence

Sequence

Sequence

Sequence

Appl

Sequence 4 Sequence 3 Sequence 3

Sequence Sequence

Sequence Sequence Sequence

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: WORD Perfect 6.1 for Windows/WS-DOS 6.2
CURRENT APPLICATION DATA:
US-08-632-470-49
US-08-938-1045-3
US-08-384-616-49
US-08-384-616-49
US-08-315-850-49
US-08-315-850-49
US-08-314-977-35
US-08-314-977-31
US-08-314-977-31
US-08-314-977-31
US-08-314-977-31
US-08-314-616-31
US-08-314-616-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
APPLICANT: APPLICANT: CANDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIASSIFICATION
PRIOR APPLICATION NAMES:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKT NUMBER: 9F-0546 US
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/09/109, 204
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-109-204-14; Sequence 14, Application US/09109204; Patent No. 6060250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 243 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-855-0572
   1494
11683
22991
22991
22991
7863
7863
7863
7917
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7917
9030
9030
9030
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: BRAINOT09
CLONE: 2150892H1
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   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA
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   TELEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                                                                                                                                                                                             RESULT
       Sequence 14, Appl Sequence 5, Appl i Sequence 213, App Sequence 214, App Sequence 215, App Sequence 213, App Sequence 214, App Sequence 213, App Sequence 214, App Sequence 214, App Sequence 213, App Sequence 214, App Sequence 213, App Sequence 202, App Sequence 20
                                                                                                                        February 20, 2002, 07:41:32; Search time 166.82 Seconds (without alignments) 23.080 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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78,
63,
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Sequence 4
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-109-204-14
US-08-9109-204-5
US-08-910-204-5
US-08-466-033-213
US-08-466-033-214
US-08-466-033-214
US-08-444-733-215
US-08-444-733-215
US-08-444-733-215
US-08-444-733-215
US-08-461-134-213
US-08-461-134-214
US-08-461-134-214
US-08-461-1361-214
US-08-461-1361-215
US-08-461-1361-215
US-08-461-1361-215
US-08-461-1361-215
US-08-461-1361-205
US-08-465-101-215
US-08-465-101-215
US-08-465-101-205
US-08-260-038-63
US-08-260-038-63
US-08-260-038-63
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                                                                                                                                                                                                                                                                                                                351203 segs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                             - nucleic search, using sw model
                                                                                                                                                                                                                                                               IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                              1 catgcattacccaccca 17
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                                                                                                                                                                                        US-09-904-420A-4
                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                               Scoring table:
                                                                                             OM nucleic
                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                             Run on:
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COUNTRY: USA
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                                           Score 15.4; DB 3; Length 243; Pred. No. 10;
                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OURENTING SYSTEM: Windows SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109.20^*
FILING DATE: HERRWITH"
                                                                          ÷
                                                                                                                                                                                                                                                                      APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Landman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gregone, Gina A.
APPLICANT: Gorgone, Gina A.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.4; DE Pred. No. 12; 0; Mismatches
                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
                                                                                                                                                                                                                           Sequence 5, Application US/09109204
Patent No. 6060250
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2125 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.6%;
94.1%;
                                             90.6%;
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Best Local Similarity 94.1'
Matches 16; Conservative
                                           Query Match
Best Local Similarity 94.1<sup>1</sup>
Matches 16; Conservative
                                                                                                           1 catgcattacccaccca 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IMMEDIATE SOURCE;
; LIBRARY: BRAINOT09
; CLONE: 2150892
US-09-109-204-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
US-09-109-204-14
                                                                                                                                                                                             RESULT 2
US-09-109-204-5
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                                                                 APPLICANT: Frudakis, Tony N.
APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 289;
                                                                                                                                                                                                                                             STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: Washington
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 11-Dec-1997
CLASSIFICATION: VUNKNOWN>
ATTORNEY/AGBNT INFORMATION:
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.4; DB 4;
Pred. No. 34;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: POLLER, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 197:
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 197:
US-08-991-789A-197/c
; Sequence 197, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.7%;
93.8%;
                                                                                                                                                             NUMBER OF SEQUENCES: 292
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Best Local Similarity 93.8
Matches 15; Conservative
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389, 886
FILING DATE: 15-FEB-1995
PRIOR APPLICATION NUMBER: US 08/357, 509
FILING DATE: 16-DEC-1994
PRIOR APPLICATION NUMBER: US 08/329, 729
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329, 729
FILING DATE: 23-NOV-1994
PRIOR APPLICATION NUMBER: US 08/285, 558
FILING DATE: 03-NOV-1994
PRIOR APPLICATION NUMBER: US 08/285, 558
FILING DATE: 03-NOV-1994
PRIOR APPLICATION NUMBER: US 08/285, 543
FILING DATE: 03-NOV-1994
PRIOR APPLICATION NUMBER: US 08/285, 543
FILING DATE: 03-NOV-1994
PRIOR APPLICATION NUMBER: US 08/285, 543
FILING DATE: 03-NOV-1994
PRIOR APPLICATION NUMBER: US 08/286, 985
FILING DATE: 10-NOV-1994
PRIOR APPLICATION NUMBER: US 08/286, 985
FILING DATE: 30-NAY-1994
PRIOR APPLICATION NUMBER: US 08/286, 985
FILING DATE: 1NFORMATION:
NAME: FEBLARY NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
THE FERNICE/TOMUNICATION INFORMATION:
THE FERNICE/TOMUNICATION INFORMATION:
THE FERNICE/TOMUNICATION INFORMATION:
THE FERNICE/TOMUNICATION INFORMATION:
                                                                                                                                                                     ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
NUMBER OF SEQUENCES: 277
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HGV-K27 VARIANT
US-08-466-033-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-08-466.033-215/c
Sequence 215, Application US/08466033;
Patent No. 5766840;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.7%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 CATGCATTCCCCACCC 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 401 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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                                                                         STREET: 350 Camb
CITY: Palo Alto
STATE: CA
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                                                                                                                                                     USA
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                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 214.7, Application US/08466033
Patent No. 5766840
GENERAL INFERMATION:
APPLICANT: Kim, Jungsuh P.
APPLICANT: Wades, John
APPLICANT: Young, Lavonne M.
APPLICANT: Young, Lavonne M.
APPLICANT: Fry, Kirk E.
APPLICANT: Fry, Hirk E.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Virus and Molecular TITLE OF INVENTION: Cloning Thereof
                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,033
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REPERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDIAL ISOLATE: HGV-7244 VARIANT
US-08-466-033-213
                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,886
FILING DATE: 15-FEB-1995
PRIOR APPLICATION NUMBER: US 08/357,509
FILING DATE: 16-DEC-1994
PRIOR APPLICATION NUMBER: US 08/329,729
FILING DATE: 26-OCT-1994
PRIOR APPLICATION NUMBER: US 08/329,729
FILING DATE: 26-OCT-1994
PRIOR APPLICATION NUMBER: US 08/344,271
FILING DATE: 23-NOV-1994
PRIOR APPLICATION NUMBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION NUMBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION NUMBER: US 08/285,543
FILING DATE: 03-AUG-1994
PRIOR APPLICATION NUMBER: US 08/285,543
FILING DATE: 20-MAX-1994
PRIOR APPLICATION NUMBER: US 08/285,543
FILING DATE: 20-MAX-1994
ATTORNEY PAGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.7%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 CATGCATTCCCACCC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.8
Matches 15: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-466-033-214/c
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Kim, Jungsuh P.

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WS-08-444-733-213/C
Sequence 213, Application US/08444733
Sequence 213, Application US/08444733
Sequence 213, Application US/08444733
Sequence 213, Application US/08444733
Sequence 213, Application CBR 24507
Sequence 213, Application Sequence 3, Application With Sequence 3, Application With Sequence 3, Application Sequence 3, Application Sequence 3, TITLE OF INVENTION: Hepatitis G Virus and Molecular TITLE OF INVENTION: Hepatitis G Virus and Molecular TITLE OF INVENTION: Cloning Thereof NUMBER OF SEQUENCES: 277
CORRESONDE DEADLESS: ADDRESS: ADDRESS: ADDRESSE: Debilinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/444,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR PAPLICATION: 435
PRIOR APPLICATION 10435
PRIOR APPLICATION NUMBER: US 08/389,886
FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,509
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,729
PRIOR APPLICATION NUMBER: US 08/344,271
FILING DATE: 23-NOV-1994
PRIOR APPLICATION NUMBER: US 08/344,271
PRIOR APPLICATION NUMBER: US 08/344,271
PRIOR APPLICATION NUMBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION NUMBER: US 08/285,543
PRIOR APPLICATION NUMBER: US 08/246,985
PRILING DATE: 20-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 466
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 350 Caml
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
APPLICANT: Wages, John
APPLICANT: Voung, LaVonne M.
APPLICANT: Fry Kirk E.
APPLICANT: Fry Kirk E.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Virus and Molecular TITLE OF INVENTION: Cloning Thereof
NUMBER OF SEQUENCES: 277
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PELLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: 10 08/389,886
FILING DATE: 15 FEB-195
PRIOR APPLICATION UNBER: 05 08/357,509
FILING DATE: 16 DEC-1994
PRIOR APPLICATION UNBER: 05 08/329,729
FILING DATE: 26 CCT-1994
PRIOR APPLICATION UNBER: 05 08/324,271
FILING DATE: 25 NOV-1994
PRIOR APPLICATION UNBER: 05 08/344,271
FILING DATE: 23 NOV-1994
PRIOR APPLICATION UNBER: 05 08/285,558
FILING DATE: 03 AUG-1994
PRIOR APPLICATION UNBER: 05 08/285,543
FILING DATE: 03 AUG-1994
PRIOR APPLICATION UNBER: 05 08/285,543
FILING DATE: 20 NOBER: 05 AUG-1994
PRIOR APPLICATION UNBER: 05 AUG-1994
PRIOR APPLICATION NUMBER: 05 AUG-1994
PRIOR APPLICATION NUMBER: 05 NOX-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,033
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 401 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fabian, Gary R. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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4600-0201.36/G100P11

ANTI-SENSE: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE: HGV-7244 VARIANT US-08-444-733-213

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Gaps

84.7%; Score 14.4; DB 1; Length 401; 93.8%; Pred. No. 35; 1ve 0; Mismatches 1; Indels

393 CATGCATTCCCACCC 378

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15; Conservative 1 catgcattacccaccc 16

Best Local Similarity

Query Match Matches ·:

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Gaps
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Pred. No. 35;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 215, Application US/08444733
Sequence 215, Application US/08444733
Factor No. 5824507
GENERAL INFORMATION:
APPLICANT: Kim, Jungsuh P.
APPLICANT: Young, LaVonne M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Hepatitis G Virus and Molecular
TITLE OF INVENTION: Hepatitis G Virus and Molecular
NUMBER OF SEQUENCES: 277
CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fabian, Gary R.
REGISTRATION UNBRER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 08/389,886
FILING DATE: 15-FEB-1995
PRIOR APPLICATION UNBER: US 08/357,509
FILING DATE: 16-DEC-1994
PRIOR APPLICATION UNBER: US 08/329,729
FILING DATE: 26-OCT-1994
PRIOR APPLICATION UNBER: US 08/344,271
FILING DATE: 23-NOV-1994
PRIOR APPLICATION UNBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION UNBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION UNBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION UNBER: US 08/285,543
FILING DATE: 20-MOMBER: US 08/285,543
FILING DATE: 20-MOMBER: US 08/285,543
FILING DATE: 20-MOMBER: US 08/285,543
FILING DATE: 10-MOMBER: US 08/285,543
FILING DATE: 20-MOMBER: US 08/246,985
FILING DATE: 10-MOMBER: US 08/246,985
          ANTI-SENSE: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE: HGV-K27 VARIANT US-08-444-733-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-NOS/MS-DOS SUSTWARE: Patentin Well.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 324-0880
(415) 324-0960
                                                                                                                                                             Query Match 84.7%;
Best Local Similarity 93.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                         393 CATGCATTCCCCACCC 378
                                                                                                                                                                                                                                                               1 catgcattacccaccc 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
Z1P: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA
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                                                      Gaps
                                                      0;
       DB 1; Length 401;
                                                      1; Indels
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TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kim, Jungsuh P.
APPLICANT: Kim, Jungsuh P.
APPLICANT: Kim, Jungsuh P.
APPLICANT: Young, LaVonne M.
APPLICANT: Fry, Kirk E.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Virus and Molecular TITLE OF INVENTION: Cloning Thereof
NUMBER OF SEQUENCES: 277
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE:
CLING DATE:
                                                        0; Mismatches
          84.7%; Score 14.4; I
93.8%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDER: 1008/389,886
FLING DATE: 15-FEB-195
PRIOR APPLICATION DATA:
APPLICATION UNDER: 05 08/357,509
FLING DATE: 16-DEC-1994
PRIOR APPLICATION UNDER: 05 08/329,729
FLING DATE: 26-OCT-1994
FRIOR APPLICATION UNDER: 05 08/344,271
FLING DATE: 23-NOV-1994
FRIOR APPLICATION UNDER: 05 08/344,271
FLING DATE: 03-NOC-1994
PRIOR APPLICATION UNDER: 05 08/285,558
FLING DATE: 03-NOC-1994
PRIOR APPLICATION UNDER: 05 08/285,543
FLING DATE: 03-NOC-1994
PRIOR APPLICATION UNDER: 05 08/285,543
FLING DATE: 03-NOC-1994
PRIOR APPLICATION UNDER: 05 08/285,543
FLING DATE: 20-NAY-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                     US-08-444-733-214/c; Sequence 214. Application US/08444733; Patent No. 5824507; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 460
                                                                                                                                      393 CATGCATTCCCACCC 378
                                                        15; Conservative
                                                                                                         1 catgcattacccaccc 16
       Query Match
Best Local Similarity
                                                           Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 214, Application US/08464134

Patent No. 5849532

GENERAL INFORMATION:
FAPPLICANT: Wages, John
APPLICANT: Young, LaVonne M.
APPLICANT: Fry, Kirk E.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Virus and Molecular:
TITLE OF INVENTION: Hepatitis G Virus and Molecular:
TITLE OF INVENTION: Cloning Thereof
NUMBER OF SEQUENCES: 277
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 18M TOTAL THE CONTRIBUTION DATA: APPLICATION NUMBER: 11S/08/464,134
FILING DATE: CLASSIFICATION: 536
PRICH APPLICATION 536
PRICH APPLICATION DATA: APPLICATION NUMBER: US 08/389,886
FILING DATE: 15-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                           4600-0201.36/G100P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.4; Di
Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                  HANTI-SENSE: NO STIGNT SOURCE: ORIGINAL SOURCE: INDIVIDUAL ISOLATE: HGV-7244 VARIANT US-08-464-134-213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 15.FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,509
FILING DATE: 16.DEC-1994
PRIOR APPLICATION NUMBER: US 08/329,729
FILING APPLICATION NUMBER: US 08/329,729
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,271
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,558
                    NAME: Fabian, Gary R.
REGISTATION NUMBER: 33,875
REPERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INCPRATION:
TELEFONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                               84.7%;
93.8%;
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                    S
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                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                    Score 14.4; DB 1; Length 401; Pred. No. 35; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 213, Application US/08464134
Patent No. 5849512
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Wages, John
APPLICANT: Fry, Kirk E.
APPLICANT: Fry, Kirk E.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Virus and Molecular TITLE OF INVENTION: Cloning Thereof
NUMBER OF SEQUENCES: 277
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/389,886
FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/357,509
FILING DATE: 16-DEC-1994
PRIOR APPLICATION NUMBER: US 08/329,729
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,271
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,271
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/285,543
FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/246,985
FILING DATE: 20-MAY-1994
                                                                                                                                                                                             ) ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HGV-K30 VARIANT
US-08-444-733-215
                                                                                                                                                                                                                                                                                                      84.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                             LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                               393 CATGCATTTCCCACCC 378
    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      Query Match 84.7
Best Local Similarity 93.8
Matches 15; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                               unknown
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                                                                                                             TOPOLOGY: unki
MOLECULE TYPE: I
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                             ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-464-134-213/c
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STATE:
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Score 14.4; DB 2; Length 401;
Pred. No. 35;
0; Mismatches 1; Indels (
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| Patent No. 5856134
| CENERAL INPORMATION:
| APPLICANT: Wages, John | APPLICANT: Young, Lavonne M. APPLICANT: Fry, Kirk E. APPLICANT: Linnen, Jeffrcy M. TITLE OF INVENTION: Hepatitis G Virus and Molecular TITLE OF INVENTION: Cloning Thereof NUMBER OF SEQUENCES: 277
| CORRESPONDENCE ADDRESS: AND ADDRESS:
APPLICATION NUMBER: US 08/329,729
FILING DATE: 26-0CT-1994
PRIOR APPLICATION NUMBER: US 08/344,271
APPLICATION NUMBER: US 08/344,271
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,588
FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,543
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,543
PRIOR APPLICATION NUMBER: US 08/246,985
FILING DATE: 20-AMX-1994
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 33,875
REPERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
TELEPHONE: CUARANTERIENTERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Parenin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,361
FILING DATE:
CLASSIFICATION: 435
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350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HGV-K30 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 CATGCATTTCCCACCC 378
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Best Local Similarity 93.8
Matches 15; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 215, Application US/08464134
Patent No. 5649532
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wages, John
APPLICANT: Young, Lavonne M.
APPLICANT: Young, Lavonne M.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Virus and Molecular TITLE OF INVENTION: Cloning Thereof
NUMBER OF SOURNCES: 277
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,134
FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                  NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFRENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
INFORMATION FOR SED ID NO: 214:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.7%; Score 14.4; E 93.8%; Pred. No. 35; Live 0; Mismatches
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STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
          FILING DATE: 03-AUG-1994

RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,543
FILING DATE: 03-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,985
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HGV-K27 VARIANT US-08-464-134-214
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APPLICATION NUMBER: US 08/389, 886
FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357, 509
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 CATGCATTCCCCACCC 378
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Best Local Similarity 93.8
Matches 15, Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: DNA. HYPOTHETICAL: NO ANTY-CO.
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Length 401;
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APPLICANT: Mages, John
APPLICANT: Voung, Lavonne M.
APPLICANT: Young, Lavonne M.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Virus and Molecular TITLE OF INVENTION: Cloning Thereof
NUMBER OF SEQUENCES: 277
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.7%; Score 14.4; DB 2;
93.8%; Pred. No. 35;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4600-0201.36/G100P11
                                                                                                                                                                                                                                                                                                                                                                    PRILING DATE: 23-NOV-1994
PRIOR PAPLICATION NUMBER: US 08/344,271
PRIOR PAPLICATION DATE:
APPLICATION NUMBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION NUMBER: US 08/285,543
FILING DATE: 03-AUG-1994
PRIOR APPLICATION NUMBER: US 08/246,985
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: HGV-K27 VARIANT US-08-461-361-214
                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/389,886
FILING DATE: 15-FEB-1995
PRIOR APPLICATION NOWBER: US 08/357,509
FILING DATE: 16-DEC-1994
                                                                                                                                                                                                                                                               FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,729
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
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                                                                                         US/08/461,361
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; Patent No. 5856134
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33.875
REFRENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324 0860
TELEFAX: (415) 324 0960
INFORMATION FOR SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 401 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 CATGCATTCCCCACCC 378
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Best Local Similarity 93.8
Matches 15; Conservative
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                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MULECULE
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-461-361-215/c
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APPLICANT: Kim, Jungsuh P.
APPLICANT: Wages, John
APPLICANT: Young, LaVonne M.
APPLICANT: Pry, Kirk E.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVEWTION: Hepatitis G virus and Molecular TITLE OF SEQUENCES: 277
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0960
INFORMATION FOR SED ID NO: 213:
SEQUENCE CHARACTERISTICS:
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SOIGITMAL SOURCE:
INDIVIDUAL ISOLATE: HGV-7244 VARIANT
US-08-461-361-213
                         PAPLICATION NUMBER: US 68/389,886
FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,509
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,729
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,271
FILING DATE: 03-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION NUMBER: US 08/285,543
FILING DATE: 105-AUX-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 214, Application US/08461361
Patent No. 5856134
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 401 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 CATGCATTTCCCACCC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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              PRIOR APPLICATION DATA:
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Best Local Similarity
Matches 15; Conserv
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STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: BAP CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATE:
APPLICATION NUMBER: US/08/461,361
FILING DATE:
CLASSIFICATION NUMBER: US 08/389,886
FILING DATE:
LING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,886
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,759
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,788
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,588
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,543
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,543
FILING DATE: 20-NOV-1994
PRIOR APPLICATION NUMBER: US 08/286,985
FILING DATE: 20-NOV-1994
ATTORNEY/AGENT INFORMATION:
TELEPRONE: 415,324-0860
INFORMATION FOR SED ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 DASE PAIR
TURCHANTION FOR SED ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 DASE PAIR
TURCHANTION FOR SED ID NO: 215:
TURCHANTION FOR SED ID NO: 315:
TURCHANTION FOR SED ID NO: 315: 316
TURCHANTION FOR SED ID
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Search completed: February 20, 2002, 07:44:41 Job Lime: 189 sec

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February 20, 2002, 07:41:32; Search time 3814.84 Seconds (without alignments) 47.886 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                      11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM nucleic - nucleic search, using sw model
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9b_gss:*
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em_gss_inv:*
em_gss_pln:*
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	BF799331	BB262580	BG386035	AW448783	U81209	AA333897	AV288928	BE148412	H12165	AQ191755	AA434578	AQ211495
	DB	11	10	11	10	11	10	10	10	11	13	10	13
	Query core Match Length DB	201	301	353	762	245	248	251	267	376	396	443	456
æ	Query	94.1	94.1	94.1	94.1	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6
	Score	16	16	16	16	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4
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BE543192 601069175 AQ697320 HS_551_B AQ4074399 HS_3155_A AA401238 zv63f03.r A1790256 uK57h08.x AQ935055 HS_5008_B BH077489 PRCI-24-3 AQ997959 PRCI-24-3 AQ997959 PRCI-24-3 AQ967401 EST377519 BE402181 CSB005C07 BE402181 CSB005C07 BE414229 SCU007.F0 AQ482035 RPCI-11-2 AQ482035 RPCI-11-2 AQ482035 RPCI-11-2 AQ4820318 RPCI-11-2 AQ507918 RPCI-11-1 BC066027 H13489 yjlse07.r1 BC066027 H3489 yjlse07.r1 BC066027 PM1-HT045 A176516 wi82c08 x AW881013 QV0-C7003 BE644683 7829411 x AQ73180 RPCI-23-4 AZ123706 RPCI-23-5 AZ123706 RPCI-23-5 AG633707 Lh71f01.x	EST 12-JAN-2001 10122 Homo sapiens CDNA, mRNA sequence. a; Craniata; Vertebrata; Euteleostomi; s; Catarrhini; Hominidae; Homo. R., Verjovski-Almeida,S., Britones,M.R., Zago,M.A., Bodin,S., Costa,F.F.,D.H. Matsukuma,A., Bala,G.S., Simpson,D.H. S., Bucher,P., Jonqeneel,C.V., O'Hare R.R., Reis,L.F., de Souza,S.J. and uman Lranscriptome with ORF expressed A. 97 (7), 3491-3496 (2000) cs Research Dr rom the FAPESP/LICR Human Cancer Genome seen in the following URL cripts/gethtml2.pl?tl=RC6&t2=RC6-CI0122 95t4=1)
BE543192 AQ697320 AAA01238 AAA01238 AAA01238 AAA01238 AAA035055 BH077489 AQ997959 AQ997959 AQ90509 BEA1799069 ANG65010 BEA179209 ANG650100 AIT19879 AIT19879 BEA114229 ANG60027 BEA14229 ANG60027 BEA14483 BEIG5646 AAM73180 AAM73180 AAM73180 AAM73180 AAM731707 ALGNMENT	
457 10 458 13 465 13 465 13 465 13 465 13 643 13 607 10 624 10 644 11 683 13 781 13 781 10 781 10 78	331 201 bp mRNA 10122-091000-021-D10 C10 331.1 GI:12128320 Sapiens yota: Metazoa; Chordata; lia; Eutheria; Primates; ases 1 to 201) Neto, E., Garcia Correa, R. M.A., da Silva, M. Jr., tein, A., deoliveira, P. S. on, A.J. un sequencing of the hum nnce Lays con, A.J. cares, F., Brentani, R. on, Sanes, F., Brentani, R. on, A.J. un sequencing of the hum nnce Lays con, A.J. cares, F., Brentani, R. on, A.J. un sequencing of the hum nnce Lays on, A.J. un sequencing of the hum nnce Lays on, A.J. telin, A.J. deoliveira, P.S. 663 lnstitute for Cancer g Institute for Cancer Renetics g Institute for Cancer Reserved tof. Antonio Prudente 10 1 +55-11-2707001 : asimpson@tudwig.org, br sequence was derived fro sequence was derived fro sequence was derived fro sett. This sentry can be se sext. This sentry can be Se
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	BE799331 RCG-CI0122-091000-021-D10 C BE799331.1 GI:12128320 EST. Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Lukaryota; Metazoa; Chordat Mammalia; Eutheria; Frimate 1 (bases 1 to 201) Dias Neto, E., Garcia Correa Nagai, M.A., da Silva, W. Jr. Goldman, G.H., Carvalho, A.F. Simpson, A.J. Shotgun sequencing of the h Simpson, A.J. Shotgun sequencing of the h Sequence tays Proc. Natl. Acad. Sci. U.S. 2020263 Contact: Simpson A.J.G. Laboratory of Canner Geneti Ludwig Institute for Cancer Rea Prof. Antonio Prudente Hrazil Tel: +55-11-2704922 Tel: +55-11-270492 This sequence was derived f Rrazil: asimpson@ludwig.org, This sequence was derived f (http://www.ludwig.org.br)
,	BET99331 LOCUS LOCUS LOCUS DEFINITION VECESSION VERSION VERSIO

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/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia propert of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed With a primer [5' GAGAGAGAGGACGAAGAGCTCTTTTTTTTTTTVV 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vortebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo
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/db_xref="taxon:10090"
/clone="A4830007A11"
/clone_lib="RIKEN full-length enriched, 10 days neonate
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG386035 353 bp mRNA EST 12-MAR-2001
602455204F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="cortex"
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1. .301
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 ATGCATTACCCACCCA 45
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BG386035
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                                                                                                                                                                                                                                                                                    source
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TITLE
JOURNAL
COMMENT
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ORIGIN
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KEYWORDS
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, S., Punda, S., Pakuda, S., Hayasa, H., Hayasa, M., Hada, A., Hayasa, M., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Hirozane, T., Hori, F., Ishikawa, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Shinagawa, A., Shiraki, T., Soqabe, Y., Suqahara, Y., Y., Shigemoto, Y., Shinagawa, A., Fahraki, T., Soqabe, Y., Suqahara, Y., Ysunoda, Y., Warahashi, F., Tominaga, N., Toya, Y., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Shide, (2000)

L. Unpublished (2000)

Contact: Yoshihide Hayashizaki
                                                                                                                                                     | 1.201 | /organism="Homo sapiens" | /organism="taxon:9060" | /organism="taxon:9060" | /organism="taxon:9060" | /organ="taxon:9060" | /organ="taxon:9060" | /organ="taxon:000" | /organ=|taxon:000" | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/,
Carninci.P., Nishiyama.Y., Wastover.A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Hermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB262580 301 bp mRNA EST 07-JUL-2000
BB262580 RIKEN full-length enriched, 10 days neonate cortex Mus
musculus cDNA clone A830007A11 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                    High quality sequence start: 16
High quality sequence stop: 201.
Location/Qualifiers
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BB262580.1 GI:8959035
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Futcleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases I to 248)

2 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

3 C.J., Lee, N.H., KIrkness, E.F., Weinstock, K.G., Gocaynen, J.D., White

3 O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

4 C.M., Fitzhudh, W.M., Fritchman, J.L., Gocahagen, N.S., Glodek, A.,

Gnime, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

4 L.M., Fitzhudh, W.M., Fritchman, J.L., Gocahagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hadohom, E., Hinkle, P.S., Jr., Kelley, J.M.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Weidman, J.F., Fitzley, R.,

Moreno-Palanques, R.F., McDonald, L.A., Nauven, D.T., Palrley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, F.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,

Hu, J.S., Greene, J.M., Grunber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,
                                                                                                                                                                                                                                                                                                                                                                          Cosmid contig and transcriptional map of three regions of human chromosome 21q22: identification of 37 novel transcripts by direct
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 245)
Guimera,J., Pucharcos,C., Domenech,A., Guimera,J., Casas,C., Solan,A., Gallardo,T., Ashley,J., Lovett,M., Estivill,X. and Pritchard
                                      U81209 245 bp mRNA EST 28-APR-1998
U81209 Human chromosome 21q22 mRNA Homo sapiens CDNA clone A4-33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA333897 248 bp mRNA EST 21-APR-1997
EST38225 Embryo, 9 week Homo sapiens cDNA 5′ end, mRNA sequence.
AA333897
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Pred. No. 1.7e+03;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21q22"
/clone="A4 33"
/clone="A4 34"
121 c 4 9 61 t
                                                                                                                                                                                                                                                                                                                                                                                                                                selection
Genomics 45 (1), 59-67 (1997)
97480716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mpritchard@iro.es
derived from YAC 238B1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Pritchard, Melanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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ilarity 94.1%;
Conservative (
                                                                                            mRNA sequence.
U81209
U81209.1 GI:2558730
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                                                                                                                                                                                              human.
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SM Trilicum aestivum

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

Triticeae; Triticum.

Triticeae; Triticum.

Triticeae; Triticum.

Triticeae; Triticum.

Triticeae; Triticum.

Clarke, B.C., Hobbs, M. and Appels, R.

Genes active in developing wheat endosperm

Lupublished (2000)

Contact: Bryan Clarke

Division of Plant Industry

C.S.I.R.O.

GPO Box 1600, Canberra, ACT, Australia

Tel: 61 2 6246 5060
                                                                                                                 /clone_lib="NIH_MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_most_="DHIO8 (phage-resistant)"
/lab_most_="DHIO8 (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oliqo-dT priming. Directionally
cloned into ECORIXAhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
callifornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
80 a 111 c 122 g
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BRY_1422 BRY Triticum aestivum cDNA clone P35-1P, mRNA sequence.
AW448783
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Pred. No. 9e+02;
0; Mismatches 1; Indels
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                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4583473"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="endosperm"
196 c 171 a
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/clone="p35-1p"
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Location/Qualifiers
       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="BRY"
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Best Local Similarity 94.1%;
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Best Local Similarity 100.
Matches 16; Conservative
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurgnathi; Muridae; Murinae; Mus.
1 (bases 1 to 251)
1 (bases 1 to 251)
2 Konno, H., Alazwa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishli, Y., Ishlkawa, T., Itoh, M., Izawa, M., Kadota, K., Kaqawa, I., Kai
C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, P., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Shibata
Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Shibata
Y., Shigemoto, Y., Shiraki, T., Tateno, M., Tannoda, Y.,
Watahiki, A., Watanabi, S., Yammura, T., Yasunishi, A., Yokola, T.,
Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
Unpublished (1999)
Contact: Yoshihide Hayashizaki
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Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Embryo, 9 week"
/dev_stage="embryo, 9 wks"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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Tel: 3018699056
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Pred. No. 1.7e+03;
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/db_xref="ATCC (inhost):135743"
/db_xref="taxon:9606"
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The Institute for Genomic Research
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Contact: Kerlavage, AR
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94.1%;
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Sasaki,N., Izawa,M., watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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MRO-HT0241-131299-002-g08 HT0241 Homo sapiens CDNA, mRNA sequence.
BE148412
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Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
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/clone="5033416606"
/clone_lib="RIKEN full-length enriched, 11 days pregnant
adult female_ovary and uterus"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ pases 1 to 267)
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/dev_stage="11 days pregnant, adult"
/lab_host="DH10b"
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/strain="C57BL/6J"
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// Sex="femile" | Sex
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ191755 396 bp DNA GSS 04-NOV-1998 HS_3228_A2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=20 Row=K, DNA sequence. AQ197755 AQ197755.1 GI:3590377
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589

Contact: Mahairas GG, Wallace JC, Hood L
High Phroughput Sequencing Center.
Iniversity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA 794: (206) 616-3618

Fax: (206) 616-3618

Email: jwallace@u.washington.edu
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1841
High quality sequence stops: 339
Source: IMAGE Consortium, LULL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1841
Seq primer: M13RPl
High quality sequence stop: 339.
Location/Qualifiers
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Pred. No. 1.7e+03;
0: Mismatches 1;
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Sequence Tagged Connector
Plate: 3228 row: K column: 20
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94.1%;
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hullman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston R., Williamson, A., Wohldman, P. and Wilson, R. Waterston Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tal: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-207001
Fax: 455-11-207001
Fax: 455-11-2707001
Fax: 455-11-2707001
Fax: 455-11-2707001
Fax: 455-11-2707001
Fax: 455-11-27001
Fax: 455-11-2700
Fax: 455
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                           Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsikuma, A., Baia, C.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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yml7e07.rl Soares infant brain 1NIB Homo sapiens CDNA clone
IMAGE:47965 5', mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/db_xref="taxon:9606"
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/dev_stage="Adult"
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Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                            AQ211495 456 bp DNA GSS 18-SEP-1998 HS_3243_A1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=9 Row=C, DNA sequence.
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BE543192 1 GI:9771837
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                                                                 Length 443;
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
T=1: (206) 616-3818
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Pred. No. 1.7e+03;
0; Mismatches 1;
                                                           Score 15.4; DB 10;
Pred. No. 1.7e+03;
0; Mismatches 1;
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/db_xref="taxon:9606"
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Sequence Tagged Connector
Plate: 3243 row: C column: 9
Class: BAC ends
High quality sequence stop: 456.
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Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                    90.6%;
94.1%;
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                                                                       Query Match 90.65
Best Local Similarity 94.15
Matches 16; Conservative
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/ Organism="Homo sapiens"
/ docume="Laxon:9606"
/ clone=lib="Soares_total_fetus_Nb2HF8_9w"
/ docume=lib="Soares_total_fetus_Nb2HF8_9w"
/ docume=lib="Soares_total_fetus_Nb2HF8_9w"
/ docume="10H108"
/ doc
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Butaryotas Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 443)

Illiar, L. Allen, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le., M., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, Washu-Merck EST project 1997

Unpublished (1997)
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0
           1. 396
/organism="Homo sapiens"
/db_rref="taxon:9606"
/clone="Plate=3228 Col=20 Row=K"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA434578 443 bp mRNA EST 29-MAY-1997 zw52b08.rl Soares_total_fetus_ND2HFB_9w Homo sapiens cDNA clone LIMAGE:773655 5' similar to TR:G1050752 G1050752 KYNURENINE/ALPHA-AMINOADIPATE AMINOTRANSFERASE;, mRNA sequence.
                                                                                                                                                                                                              /note="Organ: sperm; Vector: pBeloBACil; BAC Clones in E-Coli DH10B" 3 others
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 reve ET from Amersham
High quality sequence stop: 372.
Location/Qualifiers
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Pred. No. 1.7e+03;
0; Mismatches 1; Indels 0;
High quality sequence stop: 396.
Location/Qualifiers
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AA434578.1 GI:2139492
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Best Local Similarity 94.1%;
Matches 16; Conservative
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 465)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ774999 465 bp DNA GSS 29-JUL-1999 HS_3155_A1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=3 Row=C, DNA sequence. AQ774999.1 GI:5654727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3155 row: C column: 3
Seg primer: M13 Reverse
Class: BAC ends
library availability, please contact Pieter de Jong (pieter@dejong.med.bufalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 1107 row: J column: 13 Seq primer: T? Class: BAC ends
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/db_xref="taxon:9606"
/clone="plate=3155 Col=3 Row=C"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 458;
                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="kaxon:606"
/clone="Plate=1107 Col=13 Row=J"
/clone=lib="RPCI-11 Human Male BAC Library"
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.4; DB 13;
Pred. No. 1.7e+03;
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Location/Qualifiers
                                                                                                                                                                                                           High quality sequence stop: 458.
Location/Qualifiers
1. .458
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94.18;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Futeleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 458)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Meller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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O
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                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 457)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mall.nih.gov
Tissue Procurement: ATCC
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be tound through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov f column: 20
High quality sequence start: 7
High quality sequence start: 7
High quality sequence stop: 429.
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HS_5531_B1_E07_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1107 Col=13 Row=J, DNA sequence.
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/clone_lib="NIH_WGC_12"
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Pred. No. 1.7e+03;
0; Mismatches 1; Indels
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94.1%;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1115)

Mayer,K., Wolff,E., Clevers,H. and Ballhausen,W.G.

The human high mobility group (HMG)-box transcription factor TCF-1:
novel isoforms due to alternative splicing and usage of a new exon
                                    247361 H.sapiens T
247362 H.sapiens T
X59869 Human TCF-1
X63901 Homo sapien
X59871 Human TCF-1
AC009012 Homo sapi
AC009012 Homo sapi
AC008018 Homo sapi
AC08608 Homo sapi
                                                                                                                                                                                                          AC044846 Muss muscu
AL137077 Human DNA
AF034801 Homo sapi
1000111 Gallus gall
AC073802 Human DNA
AC079242 Homo sapi
AC073810 Homo sapi
AC073610 Homo sapi
AC073610 Homo sapi
AC02556 Homo sapi
AC02557 Homo sapi
AC02576 Homo sapi
AC02677 Homo sapi
AC022497 Homo sapi
AC022377 Homo sapi
AC072045 Homo sapi
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AC072045 Homo sapi
AC0721594 Homo sapi
AC079121 Homo sapi
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H.sapiens TCF-1 mRNA for T cell factor 1 splice form D.
247361
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C (bases 1 to 1115)
van de Wetering,M., Oosterwegel,M., Holstege,F., Dooyes,D., Suijkerbuijk,R., Geurts van Kessel,A. and Clevers,H.
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splice form D; T cell factor 1.
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AC01136
AC008018
MMTCSTF
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AL51082
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AC074389
AC011603
AC005920
AC073610
AC025256
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AY013874
AB028971
AB037821
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AC022497
AC021594
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AC022337
AC079121
AB050509
AF218066
CCS01DMG
AF218066
AC048368
LMFL3302
AX073564
AX058857
AF338109
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1 ccctcgggagcaggcagcaccccagccgcagc 35
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                              nucleic search, using sw model
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1 (bases 1 to 1165)
Mayer, K., Wolff, E., Clevers, H. and Ballhausen, W.G.
The human high mobility group (HWG)-box transcription factor TCF-Inovel isoforms due to alternative splicing and usage of a new exor
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/function="high mobility group box transcription factor"
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Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
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H.sapiens TCF-1 mRNA for I cell factor 1 splice form E.
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The human T cell transcription factor-1 gene. Structure, localization, and promoter characterization J. Biol. Chem. 267 (12), 8530-8536 (1992)
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/citation=[1]
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Ballhausen, W.G.
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/db_xref="G1:6198B4"
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LMIGSGVPGHPAATHPPAITVPPSGKOELOPFDRNLKTOAESKAEKEKFTTKFPLNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1254)
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/function="high mobility group box transcription factor"
/evidence=experimental
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Direct Submission
Submitted (28-MAY-1991) M. van De Wetering, Dept of Clinical
Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,
                                                                                                              Databasen, W.G.
Ballhausen, W.G.
Direct Submission
Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
Location/Oualifiers
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Human TCF-1 mRNA for T cell factor 1 (splice form A).
X59869 X5327 GI:36785
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DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
Suijkerbuijk,R., Geurts van Kessel,A. and Clevers,H.
The human T cell transcription factor-1 gene. Structure,
localization, and promoter characterization
J. Biol. Chem. 267 (12), 8530-8536 (1992)
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/db_xref="taxon:9606"
/tissue_type="1"-lymphoma"
/cell_type="T-lymophocyte"
/cell_lie="Jurkat"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butheria; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2855)
van de Wetering, M., Oosterwegel, M., Holstege, F., Dooyes, D.,
Suijkerbuijk, R., Geurts van Kessel, A. and Clevers, H.
The human T cell transcription factor-1 gene. Structure,
1 localization, and promoter characterization
J. Biol. Chem. 267 (12), 8530-8536 (1992)
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Van de Wetering,M., Castrop,J., Korinek,V. and Clevers,H.
Extensive alternative splicing and dual promoter usage generate
Tcf-1 protein isoforms with differential transcription control
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T-cell transcription factor; transcription factor.
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                                                                                                                                      /organism="Homo sapiens"
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96182076
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EMBO J. 10 (1), 123-132 (1991)
91114695
                                                                            Location/Qualifiers
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/gene="TCF-1"
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/gene="TCF-1"
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Van de Wetering, M.L.
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LIMLGSGYGFUAPIPATUPPBGKOELQPFDNLKTVGAESTAEREAK PTIKKPLNA
FMLYMKENRAK VI AECTLKESAAINOILGRRWHALSREEOAKYYEIARKERQLHMQLY
PGWSARDNYGKKRRRSREKHQESTTETNWPRELKDGNGGESLSMSSSSSPA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submitssion
Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical
Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,
The Netherlands
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                         The Netherlands

C (bases 1 to 1254)

van de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H.

Identification and cloning of TCF-1, a T lymphocyte-specific
transcription factor containing a sequence-specific HMG box
EMBO J. 10 (1), 123-132 (1991)
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HUMAD 7CF-1 mRNA for T cell factor 1 (splice form H).
X59870 X55329
X59870.1 GI:36787
DNA-binding protein; HMG box; T cell factor 1; TCF-1 qene.
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1.1254
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Gaps

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/product="T cell factor 1, splice form C"
/product="T cell factor 1, splice form C"
/product="101:36790"
/db_xref="G1:36790"
/db_xref="SMISS-PROT: p36402"
/
                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2910)

van de Wetering, M.

Direct Submission

Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical

Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,

The Neberlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2910)
van de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H. Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box EMBO J. 10 (1), 123-132 (1991)
                                                                                                                  17-JUN-1991
                                                                                                                                                                                                           DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
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                                                                                                                HSTCF1C 2910 bp mRNA PRI 17.

Human TCF-1 mRNA for T cell factor 1 (splice form C).
X59871 X55328
X59871.1 GI:36789
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Location/Qualifiers
1. 2910
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/clone_lib="cDNA"
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Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 35; Conservative 0; Mismatches 0
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860 c 671 g 597 t
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882 CCCTCGGGAGCAGGGCAGCACCCCCAGCCGCAGC 916
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1. 2910
/gene="TCF-1"
80. 886
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/gene="TCF-1"
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FMLYMEDRARAVIAECTLKESAAINOILGERWHALISREDOAKYYELARKERQHHMQLY
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16911. 1798,1843. 1890,2054. 2134)
/qene="TCF-1"
970. 1074
/cene="TCF-1"
970. 1074
                                                                                                                                                                                                                                                                                                           join(829. .924,970. .1074,1120. .1209,1255. .1374,1420. .1581,
1691. .1798,1843. .1890,2054. .2134)
/gene="TCF-1"
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                               Direct Submission Submitted (07-JAN-1992) M.L. Van De Wetering, Department of Submitted (07-JAN-1992) M.L. Van De Wetering, Department of Immunology, P.O. Box 8550, 3508 GA Utrecht, THE NETHERLANDS Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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/clone="phi-TCF-{5,8,11]"
/map="431.1"
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/number=6
1843.
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1891. .205
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Consensus quality: 82001 bases at least 030
Estimated insert size: 89944; sum-of-contigs estimation
Ouality coverage: 6.34 in 020 bases; pulse field gel estimation
Quality coverage: 6.34 in 020 bases; pulse field gel estimation

* NOTE: This is a "working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* the accession number will be preserved.
* the accession number will be preserved.
* 3080 34576: contig of 2979 bp in length
* 34577 59262: contig of 24586 bp in length
* 59363 76010: contig of 14648 bp in length
* 59363 76010: contig of 18648 bp in length
* 76011 79613: contig of 18648 bp in length
* 76011 79613: contig of 18648 bp in length
* 76011 79613: contig of 18648 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (03-407-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced gi:7454202.
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 84544)
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               Homo sapiens chromosome 5 clone XXpl-360D11, WORKING DRAFT
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80749: gap of unknown length
84544: contig of 3795 bp in length.
                                                                                         AC009012.3 GI:12830104
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN
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21740 c 22203 g 20376 t
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                                                                                                                                                                                                                                                                   DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.jgi.doe.gov
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Center Code: JGI
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                                            SEQUENCE, 7 ordered pieces.
                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 84544)
DOE Joint Genome Institute.
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Matches 35; Conservative
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                  Unpublished
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ORIGIN
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AUTHORS
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Summary Statistics
Consensus quality: 82614 bases at least Q40
Consensus quality: 8662 bases at least Q30
Consensus quality: 8662 bases at least Q30
Consensus quality: 86382 bases at least Q20
Estimated insert size: 89000; pulse field gel estimation
Estimated insert size: 89000; pulse field gel estimation
Estimated insert size: 80014; sum-of-contigs estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation

* NOTE: This is a "working draft' sequence. It currently
* consists of I contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* is believed to be correct as given, however the sizes
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* the accession number will be preserved.
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AC011336 86914 bp DNA HTG 23-APR-2001
Homo sapiens chromosome 5 clone CTC-250113, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                            Sequencing of Human Chromosome 5
Unpublished
Unpublished
Losses 1 to 86914)
Dob Joint Genome Institute.

Direct Submitted (06-0CT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:7710593.
                                                                                                                                                                                                                                             Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 8694)
DOE Joint Genome Institute.
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22135 c 22612 g 21422 t
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Center clone name: CIT-HSPC_250113
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/db_xref="taxon:9606"
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Matches 35; Conserv
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VERSION

COMMENT

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AC008608 200831 bp DNA HTG 20-APR-2001
Homo sapiens chromosome 5 clone CTB-113120, WORKING DRAFT SEQUENCE,
29 unordered pieces.
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Submitted (03-M0G-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced qi:7708985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 200831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 35; DB 2; Length 159420; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                       110942: contig of 15377 bp in length 111042: gap of unknown length 127290: contig of 16248 bp in length 127390: gap of unknown length 143681: contig of 16291 bp in length 143781: gap of unknown length 159420: contig of 15639 bp in length
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                                                                                                                                                                                                              contig of 6611 bp in length
gap of unknown length
contig of 13116 bp in length
gap of unknown length
                                                                      gap of unknown length contig of 7004 bp in length gap of unknown length contig of 5438 bp in length
                                                                                                                                     gap of unknown length contig of 8327 bp in length
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contig of 9325 bp in length
gap of unknown length
                            bp in length
length
                                              gap of unknown length contig of 4298 bp in length
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38414 c 39218 g 39915 t
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/db_xref="taxon:9606"
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Center Project Name: 107808, H233
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Center Code: JGI
Web site: http://www.jgi.doe.gov
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Sequencing of Human Chromosome
Unpublished
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DOE Joint Genome Institute.
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Best Local Similarity 100.
Matches 35; Conservative
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95566
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111043
127291
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33297
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TITLE
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Consensus quality: 150910 bases at least Q30
Consensus quality: 150756 bases at least Q30
Consensus quality: 150756 bases at least Q20
Estimated insert size: 156920; sum-of-contigs estimation
Coality coverage: 8.41 in Q20 bases; pulse field gel estimation
Quality coverage: 8.42 in Q20 bases; pulse field gel estimation
**NOTE: This is a "vorking draft' sequence. It currently
** consists of 26 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
                                     DNA 20-APR-2001
5 clone XXpl-929G6, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creck, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:11178048.
                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159420)
DOE Joint Genome Institute.
                                  20-APR-2001
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gap of unknown 1
contig of 158 b
gap of unknown 1
contig of 2463 b
gap of unknown 1
contig of 1268 b
gap of unknown 1
contig of 2117 b
gap of unknown 1
gap of unknown 1
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of 2499
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Center Project Name: 1189133, H51
                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                    Sequencing of Human Chromosome
Unpublished
                                                                                                                                                                                                                                                                                                                                              Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: XXp1-929G6
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Consensus quality: 186693 bases at least Q30
Consensus quality: 186693 bases at least Q30
Consensus quality: 190547 bases at least Q30
Consensus quality: 190547 bases at least Q30
Estimated insert size: 165000; pulse field gel estimation
Estimated insert size: 165000; pulse field gel estimation
Quality coverage: 7.77 in Q20 bases; sum-of-contigs estimation
(unality coverage: 6.47 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a "working draft' sequence. It currently

* consists of 29 contigs. The true order of the pieces
is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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/product="T-cell specific transcription factor"
/protein_id="CAA43658.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1790)
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2 (bases 1 to 1790)

3 (bases 1 to 1790)

4 (boosterweel.M., van de Wetering,M., Dooijes,D., Klomp,L., Minoto,A., Georgopoulos,K., Meijlink,F. and Clevers,H. Cloning of murine TCF-1, a T cell-specific transcription factor interacting with functional motifs in the CD3-epsilon and T cell receptor alpha enhancers

5 (b) 133-1142 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oosterwegel, M.A.
Direct Submission
Submitted (12-AUG-1991) M.A. Oosterwegel, Dept of Clin Immunol, Univ Hospital Utrecht, P.O. Box 85500, 3508 GA Utrecht, THE NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HMG box; T-cell specific transcription factor; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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X61385
X61385.1 G1:54760
                                                                                                                                                                                                                                                                                                                                                                                  2823 others
9 137208: gap of unknown length
9 200831: contig of 63623 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                           1. .200831

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/organism="Homo sapiens"

/chromosome="5" 2006"

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/clone="TB-113120"

/clone="TB-113120"

/clone="TB-1140" 20095 t 2823 oth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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/tissue_type="thymus"
/cell_type="T_cell"
/clone_lib="lambda Zap cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 cocotogggagcaggcagcacccagccgcagc 35
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/note="ACT splice/exon M5'
761. :984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/isolate="M2a/M5"
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100.0%;
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Best Local Similarity 100.
Matches 35; Conservative
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Consensus quality: 158956 bases at least 020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Sunday 1. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barren, B., Burkett, G., Baddwin, J., Barna, N., Bastlen, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHigh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Helin, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Leit, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McZarthy, M., McGwan, P., McGurk, A., McKernan, K., McPheeters, R., Mirova, P., McGurk, A., McKernan, K., Parere, N., McCarthy, M., McWan, P., McGurk, A., McKernan, K., Po'Donnell, P., O'Neil, D., Oliver, J., Nereson, K., Pierre, N., Palamas, J., Peterson, K., Palamas, J., Ranger, T.M., Oliver, J., Peterson, K., Pierre, N., Santos, R., Vola, Tirravers, M., Tridillo, J., Volanger, T., Viel, R., Volan, T., Travers, M., Tridillo, J., Volanger, J., Tirrell, A., Travers, M., Tridillo, J., Voland, J., Zimmer, A. and Zody, M., Taketted (12-AR-2000) Whitehead Institute/MIT Center for Genome Submitted (12-AR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:
Smit, A. F. & Green, P. (1996-1997)
                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus chromosome 11 clone RP23-46J7 map 11, WORKING DRAFT SEQUENCE, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                       0;
                                                                                                                                             Length 1790;
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Center clone name: 46_J_7

Center clone name: 46_J_7

Sequencing vector: M13; M77815; 100% of reads

Sequencing vector: M13; M77815; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 19639 bases at least (30)

Consensus quality: 156386 bases at least (30)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 11, clone RP23-46J7
                                                                                                                                             Score 26.6; DB 10;
Pred. No. 24;
0; Mismatches 4;
                                              343 t
                                                                                                                                                                                                                                                                                              245 CCTCGGGAGCAGGCAGCATCCGCAGCCTCAAC 277
                                                                                                                                                                                                                                                              3 cctcgggagcaggagcaccccagccgcage 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC044846
AC044846.2 GI:9369533
HTG; HTGS_PHASEL; HTGS_DRAFT.
/note="HMG-box"
eq. c 436 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 162496)
                                                                                                                                                      76.0%;
87.9%;
                                                                                                                                                                                                             29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
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                                                                                                                                                      Query Match
Best Local Similarity
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                                              423 a
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
AC044846/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                 BASE COUNT
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Insert size: 164000; agarose-fp
Insert size: 160296; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12242 122541; gap of 100 bp
122542 140243; contig of 17702 bp in length
140244 140343; gap of 100 bp
140344 162496; contig of 22153 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41: gap of 100 bp
97849: contig of 12108 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97850 97949: gap of 100 bp 97950 109572: contig of 11623 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109573 109672: gap of 100 bp in length 109673 122441: contig of 12769 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26860 26959: gap of 100 bp 26960 32575: contig of 5616 bp in length 32576 32675: gap of 100 bp 38781: contig of 6106 bp in length 38782 38881: gap of 100 bp 38882 44764: contig of 5883 bp in length 38882 44764: contig of 5883 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75189 75288: gap of 100 bp 75289 85641: contig of 10353 bp in length
                                                                                                                                                                                                                                                                                                                                                                      1373: contig of 1373 bp in length
1374 1473: gap of 100 bp
1474 2786: contig of 1313 bp in length
1878 2886: gap of 100 bp
2887 4262: contig of 1376 bp in length
2463 4362: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52215: gap of 100 bp
59927: contig of 7712 bp in length
60027: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59928 60027: gap of 100 bp
60028 67115: contig of 7088 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6517; gap of 100 bp
9412: contig of 2895 bp in length
9512; gap of 100 bp
10790: contig of 1278 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10890: gap of 100 bp
15080: contig of 4190 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10891 15080: contig of 4190 bp in length
15081 15180: gap of 100 bp
15181 18824: contig of 3644 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18924: gap of 100 bp 23129: contig of 4205 bp in length 2329: gap of 100 bp 26859: contig of 3630 bp in length
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75188; contig of 7973 bp in length
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1, .1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1474. .2786
/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="Laxon:10090"
/chromosome="11"
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on Mar 24, 2001 this sequence version replaced gi:13398681.

On Mar 24, 2001 this sequence version replaced gi:13398681.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following absembly was are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL: Sw:, SWISSPROT; Tr:, TREMBL: WORMPEP; Information on the WORMPEP; Hitch / August search as an abord to associate primary accession numbers given the context and the search as the found at the feature table with their source databases: Em:, EMBL: Sw:, SWISSPROT; Tr:, TREMBL: WORMPEP; Information on the WORMPEP.
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APGTPTGLPKGAAGAYTOSLGRTPTATTSGIRATLTPTVIAPRLPQPPONPTNIQNFO
LPPGMVLVRSENGQILMIPOQALAQMOAQAHAQPOTTMAPRPATPTSAPPVOISTVOA
PGTP1IARQVTPTIIKQVSQAQTTVQPSATLQKSPGVQPQILVLGGAAQTASLCTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RP11-11M20 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP5-1005F21 is at 126613 in this sequence. The true right end of clone RP5-1107C24 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="maagsDlldEvFFnSEVDEKVVSDLVGSLESQLAASAAHHHHLA
prtpEvRaaaagalgnHVVSGSPAGAAGAGPAAPARGAAAGAAPAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRPGPPSPRRPI,VPAGPAPPAAKLRPPPEGSAGSCAPVPAAAAVAAGPF;PAPAGPAKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/Chr20 an be found at http://www.sanger.ac.uk/HGP/Chr20 RP11-11M20 is from the library RPC1-11.1 constructed by the group http://www.chori.org/bacpac/home.htm
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/db_xref="GI:13559031"
                                                                  Howden, P.
Direct Submission
Submitted (23-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (23-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CEND 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2078,4728. .4847
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complement(join(965...1087,1959...2078,4728...4847,
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match: cDNAs: Em:Y11354 Fm:U75308
match: ESTs: Em:A1322519 Em:AA768928 Fm:AA023770
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 126712)
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/db_xref="taxon:9606"
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                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
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AL137077
AL137077.31 GI:13445287
HTG: CpG island; RAP55; ribosomal protein; RNA polymerase II;
RPL17; TAF2CI; TATA box binding protein; TBP-associated factor.
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Pred. No. 26;
0; Mismatches
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/note="assembly_fragment"
37212 c 36404 g 44204 t
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/note="assembly_fragment"
85742. .97849
/note="assembly_fragment"
97950. .109572
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44865. .52115

/note="assembly_fragment"

5216. .59927

/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
                                    1363. .6417
/note="assembly_fragment"
                                                                                          5518. .9412
/note="assembly_fragment"
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/note="assembly_fragment
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vector_side:right"
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84.8%;
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Best Local Similarity 84.8
Matches 28; Conservative
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repeat: matches 3689. .3980 of consensus"

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/note="L1MB7
28702. .29014
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Anote="Allu repeat: matches 1.306 of consensus"

Anote="Allu repeat: matches 129. 302 of consensus"

Anote="Allus repeat: matches 129. 302 of consensus"

12892. 13634. 12893

Anote="Allus repeat: matches 15. 157 of consensus"

Anote="Allus repeat: matches 15. 157 of consensus"

Anote="Allus repeat: matches 15. 303 of consensus"

Anote="Allus repeat: matches 1. 303 of consensus"

Anote="Allus repeat: matches 1. 303 of consensus"

Anote="Allus repeat: matches 27. 312 of consensus"

Anote="Allus repeat: matches 27. 312 of consensus"

Anote="Allus repeat: matches 1. 288 of consensus"

Anote="Allus repeat: matches 1. 289 of consensus"

Anote="Allus repeat: matches 1. 303 of consensus"

Anote="Allus repeat: matches 207. 5932 of consensus"

Anote="Allus repeat: matches 1. 363 of consensus"

Anote="Allus repeat: matches 1. 363 of consensus"

Anote="Allus repeat: matches 1. 363 of consensus"

Anote="Allus repeat: matches 1. 389 of consensus"

Anote="Allus repeat: matches 1. 389 of consensus"

Anote="Allus repeat: matches 1. 389 of consensus"

Anote="Allus repeat: matches 1. 300 of consensus"

Anote="Allus repeat: matches
                QTGTPQRTVPGATTTSSAATETMENVKKCKNFLSTL1KLASSGKUSTETAANVKELV
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/note="LlMC/D repeat: matches 4557. 5389 of consensus"
27033. 28237
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27033. .27855
                                                                                                                                                                                                               //note="Min repeat: matches 99. .158 of consensus" 8161. .8693
/note="Min2A repeat: matches 6. .453 of consensus"
                                                                                                                                                                                                                                                                                   /note="Alujo repeat: matches 5. .302 of consensus"
9270. .9587
                                                   /note="2 copies 51 mer 88% conserved"
5818. 5863
/note="23 copies 2 mer gt 97% conserved"
5920. 5977 opies 2 mer tg 89% conserved"
6091. 6148
/note="Mix repeat: main--
8181
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28253. .28360
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On 29014

Anote-"MITIAL repeat. matches 5. .365 of consensus"

Anote-"LIMITAL repeat: matches 5. .365 of consensus"

29015. .2929

On 700te-"LIMIP repeat: matches 3976. .4254 of consensus"

Complement(29342. .29857)

Gomplement(29342. .29857)

Gomplement(29342. .29857)

Anote-"ballaW20.2 (RPLI7 (60S ribosomal protein L17)

Anote-"ballaW20.2 (RPLI7 (60S ribosomal protein L17)

Fin: X60212 Em: X58389 Em: J65277 Em: EC00502 Em: X53777

Em: X60212 Em: AR204176 Em: AR0113454

Em: RE902189 Em: RA204176 Em: AR085131 Em: AR546018

Em: RE902189 Em: EW303288 Em: AR086513 Em: AR546018

Em: RE902189 Fm: R19339 Sw: C99794 Sw: P53267 Tr: C64803

Sw: C4855 Sw: P32266 Tr: C91A75 Sw: P24049 Sw: P18621

Sw: R197380 Sw: P05740 Sw: P51413 Tr: C99W3W8 Sw: P46990"
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19931. 30239

n 29931. 30239

n 29931. 30240. 30368

n 30240. 30368

n 3038. 30683

//note="LIMB7 repeat: matches 4317. 4590 of consensus"

n 3098. 32370

n 3098. 32370

n 2098. 32370

n 3098. 32373

n 3098. 32373

n 3098. 33233

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Homos sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1500)

1 (bases 1 to 1500)
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2 (bases 1 to 1500)
Serra-Pages, C. and Streuli, M.
Direct Submission
Submitted (18-NOV-1997) Tumor Immunology, Dana-Farber Cancer Institute, 44 Binney St., Boston, MA 02115, USA
Location/Oualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluJo repeat: matches 1. .296 of consensus" 33848. .33883
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Homo sapiens liprin-alpha4 mRNA, partial cds.
AF034801
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Pred. No. 44;
0; Mismatches 6;
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Db 12065 CACTCCGGAGCATGGCACCCCAGCCCCAGCCCAGC 12098
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Best Local Similarity 82.4%;
Matches 28; Conservative (
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ORIGIN
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                                                                                        /product="liprin-alpha4"
/product="liprin-alpha4"
/product="liprin-alpha4"
/protein_id="AAC26102.1"
/db_xref="Gi:3309537"
/db_xref="Gi:3309537"
/translation="SIPFSLTALSLASASPPLSGRSTPKLTSRSAAQDLDRMGVWTLP
SDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPRTLkLEKLGHPALSQEEGKSAL
EDGGSNPSSNSSQDSLHKGARKGIKSSIGRLEGKKEKGREI, DLSRDGATGHVLLTD
SEFSWQEPWYPAKLGTQAEKDREKKKHQDLEDARRKGMPFAQWCGPTVVSWLEUWVG
MPAWYVACRANVKSGAIMSALSDTEIQREIGISNALHRUKLRLAIQEMVSLTSPSAP
PTSRTSSGNVWTHEBWETLETSTKTTLAYGDMNEHATGNEWLSFGLEVQYRSYTMEC
LVDARMLDHLTKKDLRVHLKWVDSFHRTSLQYGIMCLKRLNYDRKELEKRREESQHEI
KVYLWWTNBQYVHWVQSTGLRPYAGNIHESCYHGALLALDENFDHWTLALLLLOIPTQN
TQARQVMBREFNNILLALGTDRKLDGODDKVFRRAPSWRKRFRFREHGRA"
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S Plumb, B.
Direct Submission
L Submitsed (06-7001) Sanger Centre, Hinxton, Cambridgeshire,
L Submitted (06-7001) Sanger Centre, Hinxton, Clone
requests: Clonerequest@sanger.ac.uk
On Jun 8, 2001 this sequence version replaced gj:13785420.
On Jun 8, 2001 this sequence version replaced gj:13785420.
Draft Sequence by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
Cambridge, MA 02141, USA
http://www.seq.wi.mit.edu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 200794)
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AL451082 AC02543
AL451082.3 GI:14330036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.2; DB 9; Length 1500;
Pred. No. 3.5e+02;
0; Mismatches 3; Indels 0
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Web site: http://www.sanger.ac.uk
           /organism="Homo sapiens"/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                              450 g
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Best Local Similarity 89.3%;
Matches 25; Conservative (
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AL451082/c
source
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DEFINITION
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KEYWORDS
SOURCE
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AUTHORS
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/note="assembly_fragment:02038"

/note="assembly_fragment:00744

fragment_chain:1"

15901. 169729

/note="assembly_fragment:00176

fragment_chain:1"

169830. 177240
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/note="assembly_fragment:01414"
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1. .82883
/note="assembly_fragment:00748
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fragment_chain:1"
177341. .200794
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fragment_chain:1
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50216 c 47323 g 49020 t
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89.3%; Pred. No. 98
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Job time: 14445 sec
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/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-307H16"
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Best Local Similarity
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Listing first 45 summaries
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GenCore version Copyright (c) 1993 - 2000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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			Canine-Mouse	Nucleic acid	Single nucleotide	single nucleotide			Nucleic acid	Nucleotide sequenc	Bone morphogenic p	Human ORFX ORF1288	Human cDNA encodin	RAGE-I gene.	RAGE-3 gene.	2		Human ALD gene exo	Human cDNA sequenc	-			Human TANGO 330	Hulldi Hara J Crono	ASH1	0		Human cancer assoc		Human haematopoiet

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KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; KW peripheral nervous system; neuropathy; central nervous system; CNS; KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; clienotactic; amyotrophic strong system; CNS; KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation: KW leukaemia; ss.

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26-JUL-2001.

2000US-0488725.

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25-APR-2000; 2000US-0552317.

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25-APR-2000; 2000US-0558042.

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19-JUL-2000; 2000US-053450.

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19-JUL-2000; 2000US-053450.

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19-SEP-2000; 2000US-0662191.

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29-NOV-2000; 2000US-0693036.

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09-JUL-2000;
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03-AUG-2000;
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                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                            26-DEC-2000;
                                                                                                     26-JUL-2001
                                                                                                                                                     Homo sapiens
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2000US-0552317.
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Wehrman T, X
Goodrich R,
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Xu C,
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19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                      1633
                                                                                                                                                peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
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Wang
Zhao
21-JAN-2000; 2000US-0488725
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Note: The seque
                          26-DEC-2000; 2000WO-US34263
                                                                                                                                       chemokinetic; thrombolytic;
                                                                                                                                                                                        Human;
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                                                                          WO200153312-AI
                                                                                                  Homo sapiens
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DB; AAM40719.
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2000US-0727344.
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09-JUL-2000;
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03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activiny. Inhibin activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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Wang
Zhao
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                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                      Human polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    C.N.S disorders. Note: The sequence data for this patent did not form part specification.
                       WO200153312-A1
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                                                                      leukaemia;
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DB; AAM38933.
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Wang 2
Zhou
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2000US-0598042
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Wehrman T, X
Goodrich R,
                                                                                                                              immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                                             CDNA;
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Pred. No. 34;
0; Mismatches
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RESULT 5
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AC AAC759
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19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant inmunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAI57798-AAI61369) the encoded polypeptides (AAM38642-AAM42213) with nootropic,
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                                                                                                                                 Human ORFX ORF1503 polynucleotide sequence SEQ ID NO:3005.
                                                                                                                                                                08-FEB-2001
                                                                                                                                                                                            AAC75948;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification
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Note: The sequence
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)B; AAM38932.
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as central nerv
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Wang Z,
Zhou P,
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wehrman T, J
Goodrich R,
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system injuries
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Xue AJ,
anac RT;
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Yang Y,
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RESULT 6
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The presence of the presence of the express OREX profess in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease \cdot
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                                                                                                                                                                                                                                                                                                                                                           bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance
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               AAI61340;
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                                                     AAI61340 standard; cDNA; 956
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activity, inhibit activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inilammation, leukaemias and
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Wang
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P-PSDB; AAM42184.
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19-OCT-2000;
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                                                                                                                                      disorders
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                                   Similarity
24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 5329; 10078pp; English.
                                                                                                 956
                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-062312.
2000US-0653145.
2000US-0653191.
2000US-0693036.
2000US-0727344.
                                     Conservative
                                                                                                 вP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US34263
                                                                                                  195
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Wehrman T,
                                                                                                                                      data
                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodrich R,
                                                                                                 Α,
                                               63.4%;
                                                                                                  284
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, Xu C,
                                                                                                                                    this patent did
                                     0
                                                 Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             hen R, Ma Y,
Xn C, Xue AJ,
Drmanac RT;
                                                                                                  315
                                     Mismatches
                                                 22.2;
No. 74;
                                                                                                 ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic;
                                                                                                    162
                                                             DB
                                                                                                    Ţ;
                                                                                                                                         not
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qian XB,
Yang Y,
                                                                                                    0 other
                                                                                                                                                                                                                                                                                                                                                                                for treating
                                                             22;
                                                                                                                                       form part
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                                                             Length
                                      indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ren F,
                                                               956;
                                                                                                                                         οf
                                                                                                                                                                                                                                                                                                                                                                                   disorders
                                      0;
                                                                                                                                         the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang D;
                                      Gaps
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RESULT 7 AAI59554/c

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262

CCACGCGGGAGCAGGGCACCTCCA 236

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В
                                      Matches
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypnucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as erripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                         Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cances peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI59554;
                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1757;
                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating such as central nervous system injuries -  \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI59554 standard;
                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2000;
                                                                                      Sequence
542
                                                                                                                 N.S disorders.
ote The sequer
         1 cccctcgggagcagggcagcaccccca 27
                                                                                                                                                                                                                                                                                                                                       2001-442253/47.
                                                                                                                                                                                                                                                                                                                             AAM40398
                                                Similarity
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Wang Z,
Zhou P,
                                                                                      1525
                                                                                                                  sequence
                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0488725.
2000US-0553317.
2000US-05598042.
2000US-062312.
2000US-0653450.
2000US-0663450.
2000US-0663191.
2000US-0693036.
2000US-0727344.
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                                                                                      BP;
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                                                                                                                                                                                                                                                                                                                                                                           Asundi V,
                                                                                      306
                                                                                                                                                                                                                                                                                                                                                         Goodrich
                                                                                                                   data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                88
                                                                                      Α.
                                             9.98
                                                                                                                  for this patent did
                                                                                      445
                                                                                                                                                                                                                                                                            10078pp; English.
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                                                                                                                                                                                                                                                                                                                                                         æ
                                                                                                                                                                                                                                                                                                                                                                 Chen R, Ma
Xu C, Xue
                                                                                     c;
                                               Score 22.2;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВΡ
                                                                                                                                                                                                                                                                                                                                                       hen R, Ma Y,
Xu C, Xue AJ,
Drmanac RT;
                                      Mismatches
                                                                                      509
                                                                                      ე.
                                                                                      265
                                                        DB
                                                                                      Τ,
                                                                                                                   not
                                                                                                                                                                                                                                                                                                                                                                  Qian XB,
Yang Y,
                                                        22;
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                                                                                      other;
                                                                                                                   form
                                                        Length
                                                                                                                   part of
                                                                                                                                                                                                                                                                                                                                                                   Zhang J;
                                                                                                                                                                                                                                                                                                                                                                           Ren F,
                                                         1525;
                                                                                                                                                                                                                                                                                                          disorders
                                      0;
                                                                                                                   the printed
                                                                                                                                                                                                                                                                                                                                                                             Wang
                                      Gaps
                                      0
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AAZ42266
ID AAZ4
XX
AC AAZ4
XX
AC AAZ4
XX
AT 01-F
                                                                                                                   9
                                                                                                 DЬ
                                                                                                                                       Matches
                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted
          01-FEB-2000
                             AAZ42266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC00584;
                                                                                                                                                                                      Sequence
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                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy;
                                                                                                                                                                                        271
         (first entry)
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polya+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-OT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic, forensic,
AAZ42266 standard;
                                                                                                                          2000-500381/45
DB; AAG00578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milne Edwards
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID 582; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                   BP; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; {\tt ss}\,\cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein 5' EST, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9905-0122487
  cDNA;
                                                                                                                                                                                                                                                                                                                                                                 Α,
                                                                                                                                                                                                                                                            62.3%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                   100 C;
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                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                            Score 21.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                   72 G;
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                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                            No. le+02;
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                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                                   T; 0 other;
                                                                                                                                                                                                                                                                                           DB 21;
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                                                                                                                                                                                                                                                                                        Length 271;
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                             CC AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST) CC sequences, corresponding to human secreted proteins. AAY46451 to CC AAY65438 represent the EST-related proteins corresponding to AAX42265 to CC AAZ43052. The 5' ESTs can be used for producing secreted human gene CC products. They can be used to identify and isolate 5' untranslated CC regions (UTRs) and upstream regulatory regions which control the CC location, development stage, rate, and quantity of protein synthesis, as CC well as stability of mRNA. The ESTs are also useful as probes for CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can CC also be used in forensic procedures to identify individuals, or in CC diagnostic procedures to identify individuals having genetic diseases CC resulting from abnormal gene expression. The products may also be used in CC used for directing extracellular secretion of a polypeptide or the CC used for directing extracellular secretion of a polypeptide or the CC into a cell. The proteins encoded by the EST sequences may be useful in CC treating a variety of human conditions. Secreted proteins have CC valuable. AAZ42249 to AAZ42264 and AAY664644 to AAY6450 represent XXX sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1998;
28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
gene therapy; chromosome mapping; upstream regulatory sequence;
forensic; location; development; protein synthesis; stability;
regulation; identification.
          Nucleotide sequence of a human protein having a hydrophobic domain.
                                                30-APR-2001
                                                                                   AAF25163
                                                                                                                 AAF25163 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 184-185; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                     Sequence 274 BP; 49 A; 100 C; 75 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation; identification; ss.
                                                                                                                                                                                                 94 cctcggggacagggcgccactcacagccacagc 126
                                                                                                                                                                                                                   3 cctcgggagcagggcagcacccccagccgcagc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-038446/03.
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                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                      Conservative
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated from a cDNA library SEQ ID
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98US-0069047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-IB00712
                                                                                                                 cDNA; 351
                                                                                                                                                                                                                                                                                    62.3%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A,
                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                             Pred. No. le+
                                                                                                                                                                                                                                                                                    Score 21.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                     50 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giordano
                                                                                                                                                                                                                                                                                    1e+02;
                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                    7;
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                                                                                                                                                                                                                                                                                                   Length 274;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                    Gaps
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AAV86229 ID AAV8 XX

AAV86229

standard;

cDNA; 355

Вþ QΥ

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The present sequence encodes a human protein with hydrophobic domains. CC AAP25173 represents a longer version of the present sequence. The protein possesses a hydrophobic domain and so is a secretory protein CC or a membrane protein. The protein is used as an antigen to prepare antibodies. The polynucleotide sequence is useful as a source of probes CC for genetic diagnosis. It is also useful for producing the protein CC in large quantities and for gene therapy. The enkaryotic cells are used CC for detecting the receptors or ligands corresponding to the protein and CC for detecting small novel pharmaceuticals. The antibodics are also used CC for detection, quantification and purification of the proteins. Both the CC protein and polynucleotide may be used in research or as nutritional CC sources or supplements. The protein may have cytokine and cell CC proliferation/differentiation activity, immune stimulating or suppressing activity hematopoiesis regulating activity, tissue growth activity activity, chemotactic/chemokinetic activity. Hemostatic activity and tumour inhibition activity. It may therefore may be used to treat immune deficiencies resulting from autoimmune disorders or conference in the control of the cont
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated human proteins and polynucleotides are used in research and have activities including cell proliferation/differentiation activity, immune stimulating activity and receptor/ligand activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkinson's disease; fertility; immune response; thrombosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; hydrophobic protein; secretory protein; membrane protein; sepsis; tumour inhibition; immune deficiency; autoimmune disorder; anaemia; burn; infectious disease; cancer; ulcer; periodontal disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                             Sequence 351 BP; 67 A; 136 C; 77 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 112; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-103081/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAB31673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-2000; 2000WO-JP03942
                                                                                                                                                         Local Similarity hes 26; Conserv
60
                                  3 cctcgggagcagggcagcacccccagccgcagc
cctcggggacagggcgccactcacagccacagc
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                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0194359
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/product= "hydrophobic
/note= "no termination
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1..351
                                                                                                                                                                                                62.3%;
78.8%;
                                                                                                                                                         0;
                                                                                                                                                                                           Score 21.8;
Pred. No. le
                                                                                                                                                 Mismatches
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                                                                                                                                                                                                le+02;
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                                                                                                                                                         7;
                                                                                                                                                                                                                                      Length 351;
                                                                                                                                                         Indels
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RESULT 12
AAF30027
ID AAF300
XX AAF300
AC AAF300
XX 23-APR
XX 23-APR
XX Luman
XX Luman
XX Luman
XX Inmuno
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haemostatic activity, high activity, the conditions in clivity, themostatic conditions in clivity, the activity, haemostatic and thrombolusion activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis, haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV86229;
                                                                                                                                                                                                                                                                                                                                                                                                                                     and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 165; 633pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agostino MJ, Jacobs K, Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09845435-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1999
 Human; hydrophobic domain; antiinflammatory; immunosuppressive; immunostimulant; vulnerary; antiulcer; haemostatic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1998
                                                 Human hydrophobic domain-containing protein cDNA clone HP10687
                                                                                     23-APR-2001
                                                                                                                                                     AAF30027 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 355 BP; 68 A; 136 C; 85 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                 Local Similarity 78.
nes 26; Conservative
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                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                 62.3%;
                                                                                                                                                     823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lavallie ER, McCoy JM, Treacy M;
                                                                                                                                                                                                                                                                                                   Score 21.8; DB Pred. No. 1e+02; 0; Mismatches
                                                                                                                                                     ВΡ
                                                                                                                                                                                                                                                                                                                                                                                       65 T; 1 other;
                                                                                                                                                                                                                                                                                                                                     DB 20;
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                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                       355;
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RESULT
1D AAT97082
1D AAT9
XX AAT9
AC AAT9
XX AC AAT9
XX 27-4
XX Huma
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                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        immunosuppressor, haematopoiesis regulating, tissue growth, activin, inhibin, chemotactic, chemokinetic, haemostatic, thrombolytic, receptor/ligand, antiinflammatory or antitumour thrombolytics (no evidence provided). Expression vectors, eukaryotic host cells and antibodies are also provided. The human cDNAs of the invention are used as probes for genetic diagmosis and gene sources for gene therapy, or are used in the recombinant production of the proteins. Cells expressing the secretory or membrane proteins are utilized for detection of corresponding receptors of ligands, and in candidate drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     provides human proteins (see AAB20089-96) having hydrophobic domains indicative of secretory signals and membrane domains, and nucleic acids (see AAF30020-27) encoding them. These are expected to have cell proliferation, cell differentiation, immunostimulant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of cDNA clone HP10687 encoding a human protein (see AAB20096) having a predicted N-terminal signal peptide. The clone was obtained from a human thymus cDNA library. The predicted protein has a mol.wt. of 23 kDa. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein secretion; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatotropic; thrombolytic; antitumour; antiviral; antibacterial; antifungal; gene therapy; diagnosis; membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases, inflammatory diseases, wounds, burns, incisions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New proteins with hydrophobic domains, useful for treating autoimmune diseases, inflammatory diseases, wounds, burns, incisions and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAB20096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SAGA ) SAGAMI CHEM RES CENT (PROT-) PROTEGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-2000; 2000WO-JP03944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200100824-A2
                                                                                             AAT97082 standard; DNA; 833 BP
                                                                                                                                                                                                                                                                                                                  Sequence 823 BP; 178 A; 252 C; 247 G; 146
                                                                                                                                                                            117
                                                                                                                                                                                         3 cctcgggagcagggcagcacccccagccgcagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-123008/13
                                                                                                                                                                         cctcggggacagggcgccactcacagccacagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Page 124-125; 126pp; English.
                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "the open reading frame is also specifically claimed, in Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                    62.3%;
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                                                                                                                                                                                                                                                      Score 21.8;
Pred. No. 1
                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                            149
                                                                                                                                                                                                                                                         le+02;
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                                                                                                                                                                                                                                                                                                                       T; 0 other:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunostimulant or
                                                                                                                                                                                                                                                                        Length 823;
                                                                                                                                                                                                                                            Indels
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Human haematopoietic-specific protein (HSP) DNA

27-APR-1998 (first entry)

stroke;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphoma cells (no more details). Typically, the 833 bp sequence, or bases 108-833 that encode amino acids -22 to 167 or 1 to 167 of HSP, the latter being the mature protein, is amplified from a clone deposited as ATCC 97455, and recombinant HSP is expressed in e.g. E. coli, insect, mammalian or plant host cells. The HSP (or DNA encoding it in gene therapy) can regulate differentiation and maturation of immune system cells and can thus be used to treat and protect against autoimmune disease, graft rejection, malignant cells and infection by viruses, fungi and bacteria. Fragments of HSP nucleic acids are used as diagnostic probes or primers, e.g. to detect mutalions, or for chromosome identification. Antisense sequences can be used as antagonists of HSP and used to treat or prevent daily and bacteria.
                                    AAC59795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haematopoietic-specific protein (HSP) (AAW35904), a protein that expressed specifically in thymus and haematopoietic tissues. It was isolated from a CDN disrary produced human B cells was isolated from a CDN disrary produced in the man a collegion of the colleg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding human haematopoietic-specific protein and agonists and antagonists, used for treatment and diagnosis of autoimmune disease, graft rejection, malignancies, infections and hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haematopoletic-specific protein; HSP; human; agonist; antagonist; autoimmune disease; graft rejection; malignancy; cancer; infection; hypersensitivity; therapy; diagnosis; ss.
                                                                                                                     AAC59795 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 833 BP; 200 A; 245 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This DNA sequence includes a claimed coding region for human
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                                                                                                                                                                                                                                                                                                                            101 cctcggggacagggcgccactcacagccacagc 133
                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                              3 cctcgggagcaggcagcagccccccagccgcagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 62.3%;
l Similarity 78.8%;
26; Conservative
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108..608
/*tag= c
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42..107
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42..611
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                                                                                                                     DNA;
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س
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0; Mismatches
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 833;
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17-MAR-1999;
17-MAR-1999;
17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                      haematopolesis regulation; tissue regrowth; wound healing; haemophilia; Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer; contraceptive; infection; growth inhibition; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                         01-OCT-1999;
29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted protein; human; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroi
                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                              17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  psoriasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted protein encoding
                                                                                                                                                                                                                                                                                                                  99US-0124808.
99US-0124916.
99US-0149639.
99US-0157247.
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2000US-0182711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA clone vq2 1.
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2000-638211/61.

Valenzuela D,

Yuan O,

Hoffman Ξ

> Hall J,

Rapiejko

ALPHAGENE INC

Novel proteins and polypeptides useful for the treatment of e.g multiple sclerosis, systemic lupus erythmatosus, rheumatoid arthritis, cancer, Alzheimer's disease, Parkinson's disease, stroke, anemia and

Claim 24; Page 396; 493pp; English

CC antibiflammatory, antimated by controlled antiparkinsonian, correspondencive, haemostatic, vulnerary, cytostatic, antiparkinsonian, correspondencial, virucide, and fungicide activity. The proteins and controlled antiparkinsonian, virucide, and fungicide activity. The proteins and controlled antiparkinsonian, virucide, and fungicide activity. The proteins and controlled and in research. The proteins are useful for treating immune deficiency cand disorders, which may be genetic or resulting from infections, cardinamune disorders such as multiple sclerosis, systemic lupus could deficiencies such as anaemias by regulating from infections, cardinary and replacement and for treating mycloid or lymphoid continues are also useful in compositions for bone, cardinary, tendon, citissue repair and replacement and in the treatment of wounds, incisions considered in the treatment of control and proteins are also useful in the treatment of control and control and replacement and neuropathies such as Alzheimer's and corrections of diseases and Shy-Drager syndrome, and mechanical and control and corrections and sorders such as spinal cord disorders, head trauma and control control control and control and corrections are useful for treating concert. Other uses for the protein include for inhibiting the growth, cancer. Other uses for the protein anctivity are useful for treating cancer. Other uses for the protein include for inhibiting the growth, control and control and corrected seguences with cadherin activity are useful for treating control and corrections are useful for treating cord disorders, fundi and other parasites, for effecting bodily characteristics controlled and correcteristics or repetition, strange or elimination of distance and cardiac corrects on the trial and correct and corrected and co This invention relates to 59 human secreted proteins and the nucleotide sequences encoding them. Sequences AAC59788-C59846 and AAR34687-B37745 represent the proteins and their encoding nucleotide sequences, and sequences AAB34746-B34771 represent fragments of the proteins. Probes for the DNA sequences are represented by sequences AAC59847-C59596. The proteins exhibit neuroprotective, dermatological, immunosuppressive, processing, ng, utilization, storage or elimination of dietary fat, lipid, carbohydrate, vitamins, minerals, cofactors, effecting ral characteristics, providing analgesic effects and for treat

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Best Local S
Matches 26
CC in AAAC7807 to AAC78448 encode the human cancer associated proteins given CC in AAB43398 to AAB4239. The proteins can have activities based on the CC tissues and cells the genes are expressed in Example of activities CC include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory; antityroid; antiallergic; antibacterial; antiviral; CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant; CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The CC polynucleotides and polypeptides can be used for preventing, treating or CC meliorating medical conditions and diagnosing pathological conditions. CC polynucleotides, polypeptides, antibodies, agonists and antagonists from CC immune cells, to treat disorders of haematopoietic cells, autoimmune CC disorders, allergic reactions, graft versus host disease and organ CC rejection, modulate haemostatic or thrombolytic activity, modulate
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immune disorder; haematopoietic cell disorder; autoimmune disorder;
allergic reaction; graft versus host disease; organ rejection;
haemostatic; thrombolytic; cardiovascular disorder; infection;
neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer associated gene sequence SEQ ID NO:367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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Pred. No. 1e+0
0; Mismatches
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No. 1e+02;
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                                                inflammation, cancers, cardiovascular disorders, neurological disease bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 AAC78457 and AAB44240 represent sequences used in the exemplification
                                     the
                                 present invention.
                                                                                 AAC78449
                                                          of
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Sequence 898 BP; 215 A; 258 C; 269 G; 152 T; 4 other;

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Query Match
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cctcgggagcagggcagcaccccagccgcagc 35
                         l Similarity
26; Conserv
                          Conservative
                                  62.3%;
78.8%;
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Pred. No. le+02;
0; Mismatches
                                             21;
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                                             Length
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Search completed: February 20, Job time: 12453 sec 2002, 14:31:04 Appl Appli Appli Appli Appl Appli Appli Appli Appli Appli

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                                                                                                                                                                                                                                                                                                                     Sequence
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APPLICANT: Wei et al.
TITLE OF INVENTION: Human Hematopoietic - Specific Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRNY APPLICATION DATA:
APPLICATION NUMBER: US/08/837,029
US-08-833-488B-15
US-08-833-488B-22
US-08-833-488B-23
US-08-833-488B-19
US-08-833-48BB-11
US-08-830-910-17
US-08-890-980-18
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US-08-890-990-5
US-08-890-990-5
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US-08-900-31-626-18
US-09-031-626-18
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US-09-031-626-95
US-09-031-626-95
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                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08837029 Patent No. 5945303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
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LOCATION:
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'CGD2_6/ptodata/2/ina/5B_COMB.seq:*

'CGD2_6/ptodata/2/ina/6A_COMB.seq:*

'CGD2_6/ptodata/2/ina/RB_COMB.seq:*

'CGD2_6/ptodata/2/ina/PCTUS_COMB.seq:*

'CGD2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-324-332-4
US-09-324-332-4
US-09-325-155-9
US-08-135-17-9
US-08-135-734-9
US-08-135-734-9
US-08-135-734-20
US-08-135-734-20
US-08-135-734-20
US-08-835-734-20
US-08-835-734-20
US-08-833-569B-11
US-08-833-488B-7
US-08-833-488B-7
US-08-833-488B-17
US-08-833-488B-18
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number
                                                                                                                          OM nucleic
                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                  Run on:
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No.
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APPLICANT: Miyazono, Kohei, Dijke, Peter Ten;
APPLICANT: Franzen, Petra: Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/02367

APPLICATION NUMBER: PCT/GB93/02367

APPLICATION NUMBER: GB 9224057.1

FILING DATE: No. 6207814ember 17, 1993

APPLICATION NUMBER: GB 9304677.9

FILING DATE: MARCH 8, 1993

APPLICATION NUMBER: GB 9304680.3

FILING DATE: MAY 28, 1993

APPLICATION NUMBER: 9310047.6

FILING DATE: MAY 28, 1993

APPLICATION NUMBER: 931509.2

FILING DATE: AUTY 2, 1993

APPLICATION NUMBER: 9316099.2

FILING DATE: OCCUPER: 9316099.2

FILING DATE: AUTOWNUMBER: 931809.2

FILING DATE: ACCUPER: 9316099.2

FILING DATE: ACCUPER: 9316099.2

FILING DATE: ACCUPER: 9316099.2

FILING DATE: ACCUPER: 9316099.3

APPLICATION NUMBER: 321344.5

FILING DATE: ACCUPER: 931609.3

APPLICATION NUMBER: 931609.3

ATTORNEY/AGENT INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: LUD 5298.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.6%; Score 21.2; E
Best Local Similarity 76.5%; Pred. No. 39;
Matches 26; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 77...1585
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 9, Application US/09395115; Patent No. 6271365; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2308 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-395-115-9/c
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                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cedars-Sinai Medical Center
APPLICANT: Cedars-Sinai Medical Center
APPLICANT: Toomas Neuman, Ph.D.
APPLICANT: Toomas Neuman, Ph.D.
TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO
TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF EPIDERMAL CELLS
FILLS REPERENCE: POT 41494
CURRENT APPLICANTON NUMBER: US/09/234,332A
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : NAME/KEY: gene
: LOCATION: (0)...(0)
: OTHER INFORMATION: Achoaete scute homologous protein (ASH1) gene:
: OTHER INFORMATION: Genbank accession LO8424
US-09-234-332-4
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FRANZEN, Petra
YAMSAHITA, Hidetoshi
HELDIN, Carl-Henrik
HELDIN, Carl-Henrik
INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE
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85.7%; Pred. No. 29;
Live 0; Mismatches 4; Indels 0
                                                                                     Length 833;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
STREET: 66 Flith Avenue
CITY: New York City
STATE: New York
                                                                                     Score 21.8; DE Pred. No. 25; 0; Mismatches
                                                                                                                                                                                                                                     101 cercegegacagecececacacaccacage 133
                                                                                                                                                                                          3 cctcgggagcaggcagcaccccagccgcage 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ggagcaggagcaccccagcggagc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09382256A Patent No. 6207814 GENERAL INFORMATION: APPLICANT: MIYAZONO, Kohei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09234332A Patent No. 6087168 GENERAL INFORMATION:
                                                                                     Query Match 62.3%;
Best Local Similarity 78.8%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.7
Best Local Similarity 85.7
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-382-256-9/c
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US-09-234-332-4
                  US-08-837-029-1
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Gaps

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Length 2308; Indels

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                      APPLICANT: MANDEL, Jean-Louis
APPLICANT: MANDEL, Jean-Louis
APPLICANT: AUBOURG, Patrick
APPLICANT: MOSSER, Jean
APPLICANT: SADER, Claude
TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
TITLE OF INVENTION: CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 60.0%; Score 21; DB 1; Length 152; Best Local Similarity 82.8%; Pred. No. 47; Matches 24; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,277
FILING DATE: 15-0CT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: B2272
RECEISTRATION NUMBER: B2272
TELECOMMUNICATION INFORMATION:
TELEBHONE: 703-685-0573
TELERA 248425 EMBON
TELERA: 248425 EMBON
TELERA: 248425 EMBON
SEQUENCE CHARACTERISTICS:
TRICTHRACTERISTICS:
TELERATION FOR SEQ ID NO: 9:
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STREET: 745 South 23rd Street
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Young & Thompson
STREET: 745 South 23rd Street
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: DNA (genomic) US-08-136-277-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 152 base pairs TYPE: nucleic acid
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GENERAL INFORMATION:
APPLICANT: MANDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                          COMPUTER: 14M
COMPUTER: 14M
COMPUTER: 14M
COMPUTER: Mordperfect
CURSENT PAPLICATION DATA:
APPLICATION UNBER: US/09/395,115
FILING DATE: 30-October-1995
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6271365ember-1993
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1992
APPLICATION NUMBER: 9304677.9
FILING DATE: 30-October-1993
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: 304677.9
FILING DATE: 30-Warch-1993
FILING DATE: 30-Way-1993
FILING DATE: 15-October-1993
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAWE: KOALEL, VINCER MINDER: NAME: KOALEL, VINCER MINDER: NAME: KOALEL, VINCER MINDER: NAME: NAME: KOALEL, VINCER MINDER: NAME: NAME: KOALEL, VINCER MINDER: NAME: MAME: MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 60.6%; Score 21.2; D
Best Local Similarity 76.5%; Pred. No. 39;
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ccctcgggagcagcacccccagccgcage 35
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 638-3804
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-08-136-277-9/c
: Sequence 9, Application US/08136277
: Patent No. 5644045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2308 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
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US-09-395-115-9
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FRAGMENT TYPE: inte
ORIGINAL SOURCE:
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
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Gaps

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Gaps

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DB 3; Length 152; 47; 5; Indels

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0; Mismatches
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Best Local Similarity 82.8%; Pred. No. 4
Matches 24; Conservative 0; Mismatch
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.us-08-136-277-20/c
.squence 20, Application US/08136277
.patent No. 5644045
.genERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-136-277-20
                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-835-734-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
LENGTH: 152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.0°
Best Local Similarity 82.8°
Matches 24; Conservative
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LENGTH: 702 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
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APPLICANT: AUBOURC, Patrick
APPLICANT: AUBOURC, Patrick
APPLICANT: SARDE, Claude
APPLICANT: SARDE, Claude
TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
TITLE OF INVENTION: CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Young & Thompson
STREET: 745 South & Thompson
STREET: VA
COUNTRY: USA
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                   CURRENT APPLICATION DATA: DOS GOFTWARE: PETENDON MARE: PETENDON DATA: DOS GOFTWARE: PETENDON DATA: DOS GOFTWARE: DATA: DOS GOFTWARE: DATA: DOS GOFTWARE: US/08/479,403
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: PATCH: ANGREW J: 925
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: B2272DIV
TELECOMMUNICATION INFORMATION:
STELEX: 244435 EMBON
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 GCCAGCAGGTCAGCACCTGCAGCAGCAGC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 gggagcaggagcagcaccccagcagc 35
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TELECOMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEPAX: 703-685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/479,403
FILING DATE: 07-UUN-1995
ATTORNEY/AGENT INFORMATION:
         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-835-734-9/c
; Sequence 9, Application US/08835734
; Patent No. 6013769
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: PATCH, Andrew J. REGISTRATION NUMBER: 32,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) MOLECULE TYPE: DNA (genomic) US-08-479-403-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248425 EMBON INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                         APPLICANT: MANNEL, Jean-Louis
APPLICANT: MANNEL, Jean-Louis
APPLICANT: MURORE, Patrick
APPLICANT: MOSER, Jean-
APPLICANT: MOSER, Jean-
APPLICANT: MOSER, Claude
APPLICANT: SARDE, Claude
TITLE OF INVENTION: X-LINKED ANRENOLEUKODYSTROPHY GENE AND
TITLE OF INVENTION: CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 23
ADDRESSEE: AOUNG & Thompson
STREET: 745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.0%; Score 21; DB 1; Length 702;
82.8%; Pred. No. 46;
Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/136,277
FILING DATE: 15-0CT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: PATTOT, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: B2272
TELEPHONE: 703-531-2297
TELEPHONE: 703-685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 gggagcagggagcaccccagccgcagc 35
                          68 GGCAGCAGGTCAGCACCTGCAGCAGCAGC 40
7 gggagcaggcagcaccccagccgcagc 35
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APPLICANT: Gaugler, Beatrice
APPLICANT: van den Eynde, Benoit
APPLICANT: Schrier, Peter
APPLICANT: Schrier, Peter
APPLICANT: Brouwenstlin, Nathalie
APPLICANT: Brouwenstlin, Nathalie
APPLICANT: Broom Falleur, Thierry
TITLE OF INVENTION: Complex with HIA-B7 Molecules and Uses Thereof
CORRESPONDENCE ADDRESS: 37
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,569B
                                              SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/835,734 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%; Score 21; DB 3; 82.8%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REFEISTMATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7002
                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/479,403
FILING DATE: 07-0UN-1995
ATTORNEY/AGENT INFORMATION:
NAMM: PATCH, Andrew J.
REGISTRATION WUMBER: 32,925
REFERENCE/DOCKET NUMBER: 62272DIV
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                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPAX: 703-521-2297
TELEFAX: 703-685-0573
TELEFAX: 248425 EMBON
INFORMATION FOR SEQ. ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-835-734-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.0
Best Local Similarity 82.8
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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            GS-08-479-403-20/c

S Sequence 20, Application US/08479403

Patent No. 5869039

GENERAL INFORMATION:
APPLICANT: MANDEL, Jean-Louis
APPLICANT: AUBOUNG, Patrick
APPLICANT: AUBOUNG, Patrick
APPLICANT: ASTE, Claud
TITLE OF INVENTION: X-LINED ADRENOLEUKODYSTROPHY GENE AND
TITLE OF INVENTION: CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Young & Thompson
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Patent No. 6013769
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MANDEL, Jean-Louis
APPLICANT: MUSSER, Jean
APPLICANT: MUSSER, Jean
APPLICANT: STRE, Claude
TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
TITLE OF INVENTION: CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,403
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: B2272DIV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME. 703-521-2297
TELEFAX: 703-685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 2;
Pred. No. 46;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
2IP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Young & Thompson
STREET: 745 South 23rd Street
CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                      E: Young & Thompson
745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.0%;
Best Local Similarity 82.8%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 248425 EMBON INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: 1i;
; MOLECULE TYPE:
US-08-479-403-20
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US-08-835-734-20/c
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Gaps

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Indels

Gaps

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GENERAL INFORMATION:
APPLICANT: Gaugler, Beatrice
APPLICANT: van den Eynde, Benoit
APPLICANT: Schrier, Peter
APPLICANT: Brouwenstijn, Nathalie
APPLICANT: Brouwenstijn, Nathalie
APPLICANT: Broon-Falleur, Thierry
TITLE OF INVENTION: Isolated RAGE-1 Derived Peptides Which
TITLE OF INVENTION: Complex with HLA-B7 Molecules and Uses Thereof
NUMBER OF SEQUENCES: STATE OF THE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1311;
   Length 1235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: Federal Reserve Plaza, 600 Atlantic Avenue CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC:DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,569B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 2;
Pred. No. 46;
0; Mismatches
      Score 21; DB 2;
Pred. No. 46;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           998 GGCCCAGGCAGCACCAGAGCCCCGGC 970
                                                                                                                                                                     922 GGCGCAGGCAGCACCCAGAGCCCCGGC 894
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                                                                                                                                 7 gggagcaggaagcaccccagccgcagc 35
                                                                                                                                                                                                                                                                                               RESULT 13
US-08-530-569B-1/c
; Sequence 1, Application US/08530569B
; Patent No. 5939526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REPERROEX/ORGET UNMBER: L0461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-808-346-3/c
; Sequence 3, Application US/08808346
; Patent No. 6251671
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%;
82.8%;
             60.0%;
82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1311 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-08-530-569B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.09
Best Local Similarity 82.89
Matches 24; Conservative
                   Query Match 60.03
Best Local Similarity 82.83
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gaugler, Beatrice
APPLICANT: Gaugler, Beatrice
APPLICANT: Schrier, Peter
APPLICANT: Schrier, Peter
APPLICANT: Brouwenstijn, Nathalie
APPLICANT: Broom-Falleur, Thierry
TITLE OF INVENTION: Complex with HIA-B7 Molecules and Uses Thereof
TITLE OF INVENTION: APPLICANT WITH HIA-B7 MOLECULES AND CORRESPONDENCES: 37
CORRESPONDENCE ADDRESS: ADDRESSE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREEF: Federal Reserve Plaza, 600 Atlantic Avenue CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,569B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.0%; Score 21; DB 2; Best Local Similarity 82.8%; Pred. No. 46; Matches 24; Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Gates, Edward R.
RECISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7002
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HI HIHIHIHIHI HIHI HIH HI B85 GGGGGCAGGCACCCAGC 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 gggagcagggagcaccccagccgcagc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-530-569B-12/c; Sequence 12, Application US/08530569B; Patent No. 593526; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-3441
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1168 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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US-08-530-569B-11
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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Gaps

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Search completed: February 20, 2002, 14:32:32
Job time: 14411 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-833-488B-6
                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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APPLICANT: Hogan, Brigid L.M.
TITLE OF INVENTION: Compositions and Methods of Making
TITLE OF INVENTION: Embryonic Stem Cells
NUMBER OF SEQUENCES:
ADDRESSE: Panitch Schwarze Jacobs & Nadel, P.C.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Proppy disk
COMPUTER: Proppy disk
COMPUTER: PLOSSYMS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,346 FILIG DATE: 28-FEB-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08833488B
Patent No. 6060326
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Rushlow, Keith E.
TITLE OF INVENTION: Method to Detect Canine IgE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
STREET: Fort Collins
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 59.4%; Score 20.8; I
Best Local Similarity 78.1%; Pred. No. 53;
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/833,488B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 9823-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 831-494
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2183 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-833-488B-6/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xaa = unknown amino acid
60
FILING DATE: 07-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-3
TELEPOMUNICATION INFORMATION:
TELEPAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 591 nucleotides
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.9%;
Best Local Similarity 74.3%;
Matches 26; Conservative
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179
                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                              linear
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280 Contact: Kerlavage, AR
                                                                                                                                                                                                                         AA311787 273 bp mRNA EST 19-APR-1997 EST182503 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to Aa311787 AA311787.1 GI:1964114
                                                                                                                                                                                                   ALIGNMENTS
A1124575
B1403328
A1217274
B1607375
A2850363
BF303935
BF944451
BF95325
AJ284096
BF95325
                                                                                                                               AV630095
AA935860
BI164168
                                                                             AL541947
CNS03VF4
BI390398
                                                                                              AI434403
BI340223
BG715648
                                                                                                                                                                W24845
AW404274
BB584341
BE246824
                                                                   BF846035
BG014392
                                                                                                                    AQ846434
AA973990
                                                                                                                                                 AA988946
BE050797
                                                                                                                CNS03Y7H
                                                                                                                                                            BG029934
 human.
 RESULT 1
AA311787
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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BG655601 ia84a02.x
BG38035 602455204
AW872092 db22c01.y
AU007753 AU007753
B1349635 dae61e11.
B1134476 602904810
AL589082 AL589082
BG712238 pg11n.pk0
A158159 mr9803c09.x
AA155158 mr9803c0.x
                                                (without alignments)
99.150 Million cell updates/sec
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                                         February 20, 2002, 13:52:34; Search time 3793.25 Seconds
                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                   22703874
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                           35
                                                                             1 ccctcgggagcaggcagcaccccagccgcagc
                                                                                                        11351937 seqs, 5372889281 residues
                                                                                                                   hits satisfying chosen parameters:
                                                             US-09-904-420A-1_COPY_882_916
                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                              BG386035
AW872092
AU300753
B134476
B1154476
AL589082
BG712238
AA126359
AA126359
                                                                                                                                                          summaries
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BG655601

    nucleic search, using sw model

                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 st
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gb_est1:*
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em_gss.*
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em_gss_rod:*
em_gss_vrt:*
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em_gss_pln:*
                                                                                                                              seq length: 0
seq length: 200000000
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em_esthum: *
em_esthun: *
em_estpl: *
em_estpl: *
em_estpl: *
em_estpl: *
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3353
3353
3229
3312
649
649
573
673
497
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Match 1
                                                                                                                                                                     EST:*
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76.0
75.4
72.6
72.6
72.6
71.4
69.1
66.9
66.3
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226.4
225.4
225.4
24.2
24.2
23.4
23.4
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                                                                                        Scoring table:
                                                                        Perfect score:
                                                                                                                              Minimum DB
Maximum DB
                                 nucleic
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AL26958 Tetraodon AQ866434 LMAJFV1_1 AA973990 qqq3111.5 AA670095 AV630095 BI164168 KE03778.5 BI164168 CON16402.8 BE050797 Za69f03.D BG029934 602297278 W24845 Zb63712.r1 AW404274 U1-HF-BLO

BE246824 TCBAP1E51

RCO-HT093 PM1-EN006 PM3-GN030 AL541947

pgplc.pk0 til4a01.x 365433 MA 602675992

AT434403 BT340223 BG715648

Tetraodon

BG014392 AL541947 AL262345 BI390398

Sequence:

Run on:

Searched:

Database

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RC5-NN116 MR3-GN018 RC5-NN116 4A3B-AAI-RC3-NN019

BF955325 BAJ284096 4 BE934586 B

A1217274 GB1067375 FA2850363 DBF303935 GBF944451 FBG002207 N

; 0

Gaps ..

Indels

4

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/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
Cloned into EcoRI/XhoI sites using the tollowing 5'
adaptor: GGACGAG(G). Size=selected 5500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Siratagene) and Superscript II RF (Life Fechnologies)"
80 a 111 c 122 g 40 t
                                                                                                                                                   /note="Organ: Pancreas; Vector: pZEro-2; Site_1: NotI; Site_2: XhoI; Library constructed using SuperScript plasmid Library kit (Life Technologies). cDNA made by obligo-dr priming. XhoI site destroyed during cloning. Size-selected by column fractionation; average insert size 1.2kb. Primary library, unamplified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unpublished (1727) used to force the contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
Tissue Procurement: ATCC
TONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1307 row: h column: 02
High quality sequence stop: 276.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG386035 353 bp mRNA EST 12-MAR-2001
602455204F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4583473 5',
/db_xref="taxon:10090"
/clone_lib="Melton Mouse E16 5 Pancreas Library M1621"
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                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 400;
                                                                        /tissue_type="Total pancreas"
/dev_stage="Embryonic day 16.5"
/lab_host="TOP10"
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Best Local Similarity 87.9%; Pred. No. 75;
Matches 29; Conservative 0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:4583473"
/clone_lib="NIH_MGC_15"
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                                                             /sex="Both"
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Schmitt, A., Martin, J., Bilter, B., Martin, J., Blitter, S., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Milliams, T., Tadason, T., and Bovers, Y.

Unpublished (2000)
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
                                         The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 781: 3018699035 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hqi/hqi.html) Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG655601 400 bp mRNA EST 05-JUL-2001 ia84a02.x1 Melton Mouse E16 5 Pancreas Library M16x1 Mus musculus cDNA 3' similar to SW:TCF1_MOUSE 000417 T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="ATCC (inhost):158998"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI: Site_2:
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Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 35; Conservative 0; Mismatches 0;
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/strain="ICR"
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                                                                                                                                                                                                                                                                                           Location/Qualifiers
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BG655601.1 GI:13793010
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                                      Bioinformatics
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/GLORD="spoot 4896"
/GLORD="spoot 4896"
/Clone="spoot 459"
/Clone="spoot 459"
/Clone="lip="schizosaccharomyces pombe late log phase CDNA"
/Sex="h minus"
/note="vector: M13mp19: The CDNA library of
schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The CDNA data of
schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
a
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidoa; Pipidae;
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Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
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                                                            Gaps
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                                                                                                                                                                                                                                                                                                                AUGO7753 312 bp mRNA EST 31-JUL-1998
AUGO7753 Schizosaccharomyces pombe late log phase CDNA
Schizosaccharomyces pombe CDNA clone spc02459, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Contact: Mitsucki Morimyo
Contact: Mitsucki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inagerku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nits.go.jp.
1.312
| .312|
/ organism="Schizosaccharomyces pombe"
/ strain="Schizosaccharomyces pombe"
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   Length 229;
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82.9%; Pred. No. 1.7e+02;
tive 0; Mismatches 6;
Score 25.4; DB 10;
Pred. No. 1.7e+02;
0; Mismatches 6;
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AU007753.1 GI:3344211
         72.6%;
82.9%;
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Xenopus laevis
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BI349635
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         Query Match
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Matches 29; Conserv
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AU007753/c
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VERSION
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Khol; cDNA was prepared from 2ug of poly A+ RNA.

RCORT-Xhol cut cDNA was then ligated into Unizap-XR (Stratagene) with EcoRI at the 5' end and Xhol at the 3' end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization to biothnylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sephacose chromatography, the SS-phagemids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Normalized by Jihwan Song (Song, Cho and Blumberg) unpublished). Note: This is a Xenopus Gene Collection (XGC) library.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                         db22c01.y1 Xenopus laevis oocyte Xenopus laevis cDNA clone XENOPUS_SOURCE_ID: 5', mRNA sequence.
AW872092
EST.
                                                      Gaps
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                                                      1; Indels
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/db_xref="taxon:8355"
/clone="xENOPUS_SOURCE_ID:"
/clone=lib="xenopus laevis oocyte"
/tissue_type="oocyte (stages 5 and 6)"
/lab_host="Top-10 F"
                           Pred. No. 86;
0; Mismatches
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Location/Qualifiers
                                                                                                             Best Local Similarity 96.4%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    African clawed frog.
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Not1: Site_2: Sal1; Cloned unidirectionally, Primer: Oligo dT. Site_2: Sal1; Cloned unidirectionally, Primer: Oligo dT. Average insert 2 kb. Library constructed by Life actalog insert 2 kb. Library constructed by Life actalog a 12017-018. Investigators providing rechnologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: This is a NCL_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (bases 1 to 573)
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GCGCCCGCTTTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
(*6854-
                                                                                    Ph.D.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.C
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.C
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.C
Tissue Procurement: Link. Hennighausen Ph.D., Chu-Xia Deng Ph.C
Tissue Procurement: Link. Hennigh Timc, Chong Timc, DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the Link. A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LiAMI1095 row: d column: 03
High quality sequence stop: 647.
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AL589082 BP Chicken Brain Library Gallus gallus cDNA clone
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84.8%; Pred. No. 2.38+02;
Live 0; Mismatches 5; Indels
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/db_xref="taxon:901"
/clone="RoSO8Babo"
/clone="Bp-"Bp-Chicken Brain Library"
                                                                                                                                                                                                                                                                                                                                                                                                                               1. 649

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:5034194"

/clone="IMAGE:5034194"

/clone=Lib="NHLCGAP_Mam3"

/tissue_type="tumor, gross tissue"

/lab_host="DH108"
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BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
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Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
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Best Local Similarity 84.8
Matches 28; Conservative
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                                   Xenopodinae; Xenopus.

I (bases 1 to 639)

S. Lifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D. Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Person, Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B.Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Washu Xenopus. B.T. project, 1999

Unpublished (1999)

Londact: Sandy Clifton, Ph.D.

Washu Xenopus BST project, 1999

Washington University School of Medicine

4444 Porest Park Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Famil: est@watson.wustl.edu
Library constructed by Bento Soares and M. Fatima Bonaldo
Library constructed by Bento Soares and M. Fatima Bonaldo
(University of Iowa). DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
High quality sequence stop: 432.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Enmanalia; Eutherla: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 649)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:8355"
/clone="IMAGE:4678748"
/clone_lib="Blackshear/Soares normalized Xenopus egg
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/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
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B1154476
B1154476.1 GI:14614477
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1880920"
/clone="IMAGE:1880920"
/clone=lib="oracinoid"
/clone_lib="oracinoid"
/lab_host="Mall08"
/note="Organ: lung, Vector: pT773D-pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from modified polylinker: 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco R1 adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco R1 sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                 Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 67)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-OGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   ;, mRNA
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similar to SW:ASH1_HUMAN P50553 ACHAETE-SCUTE HOMOLOG 1.
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81.8%; Pred. No. 6.9e+02;
Live 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnj.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trace considered overall poor quality Insert Length: 634 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 ccgcgcgcgccgccagccccagccgcagc 10
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                                                                        A1268359.1 GI:3887526
                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 81.8
Matches 27; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Enteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
E 1 (bases 1 to 587)
S Burnside,J., Morgan,R.W. and Cogburn,L.A.
Chicken ESTS from a normalized liver library
Confact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-3341
                                                                                                      0;
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pglln.pk011.k12 Normalized Liver Library Gallus gallus cDNA clone
pglln.pk011.k12 5' similar to no significant hits (pLog(P) 4)G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1268359 67 bp mRNA EST 29-JAN-1999
qm05a09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone 1MAGE:1880920 3'
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                                                                                                                                                                                                                                                                                                                                                               Score 24.2; DB 10; Length 573;
Pred. No. 4.1e+02;
0; Mismatches 3; Indels 0;
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/db_xref="taxon:9011"
/clone="pqlln.pk011.k12"
/clone_lib="Normalized Liver Library"
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: joan@UDel.Edu, www.chickest.udel.edu.
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/lab_host="E.coli EMDH108"
/note="Vector: pcMvSPORT 6"
152 c 165 g 150 t
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                                                      /dev_stage="Unknown"
/lab_host="DH10B"
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                                    /tissue_type="Brain"
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89.7%;
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Matches 26; Conservative
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BG712238
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Matches 26; Conserv
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/tissum_type="pooled frontal lobe"
/tissum_type="pooled frontal lobe"
/tev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: brain; Vector: Bluescript SK-; Site_1: EcoRI
/stanley Neuropathology Consortium (www.stanley]ab.org)
brains S-58, S-65, S-778. Random + oligo-dT primed
into EcoRI site of ZAP 11 Vector: Mass excised. Avg
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I ( bases 1 to 462)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lary,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu
plate: 2145 row: P column: 14
Seg primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 457.

1. 457
                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="tacon:5606"
/clone="Pitacon:5606"
/clone="tace-2145 Col-14 Row=p"
/clone="lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40n13 fwd. Er from Amersham
High quality sequence stop: 427.
                                                                                                                                                                                                                                                                                                             /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
Mashington University School of Medicine
Tel: 314 Park Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 457;
                                                                                                                                                                                                                                                                                                                                                                  2 others
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/clone_lib="Johnston frontal cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23.2; DB 13;
Pred. No. 8.1e+02;
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/db_xref÷"taxon:9606"
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AI124575.1 GI:3593089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.3%;
89.3%;
                                                                                                                                                                                                                                                                                                 /sex="male"
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Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Stratagene mouse embryonic carcinoma (#937317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ877378 457 bp DNA GSS U9-NOV-1999 HS_2145_B2_H07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2145 Col=14 Row=P, DNA sequence.
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                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGG:370881
Seq primer: -28ml3 revl ET from Amersham
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                 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
                                                                                                                                                           Confect: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:605449"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="carcinoma"
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                                                                                                                 The WashU-HHMI Mouse EST Project
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//acce-most-masses modely vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NHLL19W, testis NHT, and B-cell lung NHLL19W, testis NHT, and B-cell vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 294480-302087, 682632-687239, 726409-728711, and 729096-731399. Subtraction by Bento Soares and M. Fallma Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                   A1217274 562 bp mRNA EST 30-NOV-1998 gh25a01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845672 3' similar to gb:305392 SYNDECAN-1 PRECURSOR (HUMAN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Caucer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index Under Contact Servine Annatomy recject (Contact Robert Strausberg, Ph.D. Email: cgapbs-femail.nih.gov
This clone is available royalty-free through LinL; contact the IMAGE Consortium (info@image.linl.gov) for further information. Insert Length: 1019 Std Error: 0.00
Seq prime: -400P from Gibco____
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High quality sequence Stop: 255.
Location/Qualifiers
1. 562
Corganism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Inba"Soares_NFL_T_GBC_SI"
/lab_host="DH108"
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0; Mismatches 7;
                                                                       Score 22.8; DB 11;
Pred. No. 1.1e+03;
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// Ab xref="Laxon:9823"
// Clone="MI-P-CPI-nwi-c-10-0-UI"
// Lone="WI-P-CPI-nwi-c-10-0-UI"
// Lone="WI-P-CPI"
// Lone="WI-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoLI site and the oligo-dT track served to verify it as a clone from the normalized uterus library properation. M.B. Soares Lab University of Iowa EST sequencing: M.B. Soares Lab Clowa Clone distribution: clones will be available through Research Seq primer: MI3 Forward
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insert length 1.9kb. Custom library provided by Dr. Nancy Johnston [(410) 614-3918, nlj@welchlink.welch.jhu.edu].
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 497)
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Normalization and subtraction: two approaches to facilitate gene
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Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Feat: 5152944252
Fax: 5152942401
Email: cktuggle@lastate.edu
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Pred. No. 8.1e+02;
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/organism="Sus scrofa"
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TAG_TISSUE=uterus
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Best Local Similarity 89.3%;
Matches 25; Conservative
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  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                           1472140 segs, 8248589755 residues
                                                              US-09-904-420A-1_COPY_866_900
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                            - nucleic search, using sw model
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Maximum Match 100%
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AC073405 AC091039 AC068125 AP003065 AC023176

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AF72532 Hepatitis AF172535 Hepatitis AF15515 Hepatitis AF065200 Homo sapi AC008529 Homo sapi AC008521 Homo sapi AC07822 Mus muscu AC022298 Mus muscu AC022298 Homo sapi AC022398 Homo sapi AC022298 Homo sapi AC022398 Homo sapi AC022398 Homo sapi AC022096 Homo sapi AC069075 Mus muscu

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AC011336 AC009017 AC008608 HSTCF1C AC009012

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28.

HSTCF1D HSTCF1E HSTCF1A HSTCF1B

DB

Length

Query Match

Score

AC022298

10

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Mus muscu

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

JOURNAL REFERENCE AUTHORS

Function Sapiens

Bukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Calarrhini; Hominidae; Homo.

1 (bases 1 to 115)

Mayer, K., Wolff, E., Clevers, H. and Ballhausen, W.G.

The human high mobility group (HMG)-box transcription factor TCF-1:

The human high mobility group (HMG)-box transcription and usage of a new exon Unpublished to 2007 (2.4 pages, F., Dooyes, D., van de Weetring, M., Oosterwegel, M., Holstege, F., Dooyes, D., suijkerbuijk, R., Geurts van Kessel, A. and Clevers, H.

ALIGNMENTS

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Direct Submission
Submitted (28-MAY-1991) M. Van be Wetering, Bept of Clinical
Immunology, University Hospital, P.O. Box #5500, 4508 GA Utrecht,
                                                                                                                                                                                                                                                                                                                                                                                                                                 /citation=[1]
/function="high mobility group box transcription factor"
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                                                                                                                                                     Direct Submission
Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Iniversitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1. (bases 1 to 1254)
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Human TCF-1 mRNA for T cell factor 1 (splice form A).
X59869 X5327
X59869-1 G1:46785
DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
Suijkerbuijk,R., Geurts van Kessel,A. and Clevers,H. The human T cell transcription factor-1 gene. Structure, localization, and promoter characterization J. Biol. Chem. 267 (12), 8530-8536 (1992)
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Best Local Similarity 100.0%;
Matches 35; Conservative 0;
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Ballhausen, W.G.
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1 (bases 1 to 1165)

Mayer, K., Wolff, E., Clevers, H. and Ballhausen, W.G.

The human high mobility group (HMG)-box transcription factor TCF-1:

novel isoforms due to alternative splicing and usage of a new exon
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/evidence=experimental
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Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
Location/Qualifiers
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van de Wetering,M., Oosterwegel,M., Holstege,F., Duoyes,D.,
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            The human T cell transcription factor-1 gene. localization, and promoter characterization biol. Chem. 267 (12), 8530-8536 (1992)
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Ballhausen, W.G.
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AUTHORS
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Gaps

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.
1 (basea: 1 to 2855)
van de Wetering, M., Oosterwegel, M., Holstege, F., Dooyes, D.,
Suijkerbuijk, R., Geurts van Kessel, A. and Clevers, H.
The human T cell transcription factor-1 gene. Structure,
10calization, and promoder characterization
3. Biol. Chem. 267 (12), 8530-8536 (1992)
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Extensive alternative splicing and dual promoter usage generate
Tcf-1 protein isoforms with differential transcription control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1999
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                                                                                                                                                            /organisme"Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T lymphocyte"
/cell_line="Jurket and HPB-ALL"
/clone_lib="cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell. Biol. 16 (3), 745-752 (1996)
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831 c 648 g 572
                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=experimental
EMBO J. 10 (1), 123-132 (1991)
91114695
                                                                                                         Location/Qualifiers
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/gene="TCF-1"
80. .889
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/qene="TCF-1"
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/qene="TCF-1"
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                                                                               See also X59869-X59871
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Best Local Similarity 100.
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/product=rT cell factor 1, splice form A"
/product=rT cell factor 1, splice form A"
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/db_xref=rGI:36786.1"
/db_xref=rGI:36786.1"
/db_xref=rSMS-PROT:P36402"
/db_xref=rSMS-PROT
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                                                      2 (bases 1 to 1254) van de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H. Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box EMBO J. 10 (1), 123-132 (1991)
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DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
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Muman TCP-1 mRNA for T cell factor 1 (splice form B).
X58870 X55329
X59870.1 GI:36787
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391 c 335 g 208 t
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                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T lymphocyte"
/cell_line="Jurkat"
/clone=lib="cDNA"
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/gene="TCF-1"
/note="HMG box"
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                                               rhe Netherlands
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/translation="myketvysarnilmhypppsgacohpopplikanopphgvpo
ISINEHFNSPHPTPARADISOKOVHRPLOTPDISGYSYLSGSMGQLPHTVSMRTHPS
LIMGSGVPGHPAAIPHPAIPHPAIPHSPSKOELOPFDRNLKTOAESKARKEAKKPTIKPLNA
EMLYMKEMRAKVIAGCTLKESAAINOILGRRWHALSREBOAKYFLARKEROLHMOLY
POGNSARDNYGKKKRRSKEKHOESTTDPGSPKKCRARFGILNOQTDWGGPCR"
                                                                                                                                                                                                                                                                                    Homo sapiens
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2910)
van de Wetering, M.
Direct Submission
Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical
Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical
Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,
The Netherlands
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van de Wetering,M., Oosterwegel,M., Dooijes,D. and Clevers,H.
Identification and cloning of TCF-1, a T lymphocyte-specific
transcription factor containing a sequence-specific IMG box
EMBO J. 10 (1), 123-132 (1991)
91114695
See also X59869-X59871.
                                                                                                                            17-JUN-1991
                                                                                                                               HSTCFIC 2910 bp mRNA PRI 17-JUN-1'
Human TCF-1 mRNA for T cell factor 1 (splice form C).
X59871 X55328
NS9871.1 G1:36789
DNA-binding protein; HMG box; T cell factor 1; TCF-1 gene.
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/product=Tr cell factor 1, splice form C"
/protein_id="CaA4258.1"
/db_xref="GI:36790"
/db_xref="SWISS-PROT:P36402"
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100.0%; Score 35; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 35; Conservative 0; Mismatches 0;
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Location/Qualifiers
1. 2910
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/db_xref="taxon:9606"
/cell_Lype="T lymphocyte"
/coll_line="Jurkat and HPB-ALL"
/clone_lib="conna"
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597
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/evidence=experimental
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80. .886
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/gene="TCF-1"
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                                                                                                                                                                                                                                                                                                                           join(829. .924,970. .1074,1120. .1209,1255. .1374,1420. .1581, 1691. .1798,1843. .1890,2054. .2134)
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                   Direct Submission
Submitted (07-JAN-1992) M.L. Van De Wetering, Deparlment of
Immunology, P.O. Box 8550, 3508 GA Utrecht, THE NETHERIANDS
Location/Qualifiers
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                                                                                                                    1. .2855 "Homo sapiens" 
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829. .924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB56795.1"
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/number=1
970.
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929 c
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2054. .213
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1891. .209
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Gaps

HTG

DNA

84544 bp

AC009012

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consensus quality: 82614 bases at least Q40
Consensus quality: 85602 bases at least Q30
Consensus quality: 8632 bases at least Q30
Consensus quality: 8632 bases at least Q20
Consensus quality: 8632 bases at least Q20
Estimated insert size: 86910; pulse field gel estimation
Duality coverage: 6.4 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs estimation.

* is believed to be correct as given, however the pieces

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Totalis will be contig of 86914 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
(pases) to 86914)

Constitute.

Doc Joint Genome Institute.

Direct Submission
Submitted (06-0CT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced 91:7710593.
                                                                                                                                                         AC011336 86914 bp DNA HTG 23-APR-2001
Homo sapiens chromosome 5 clone CTC-250113, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 86914)

DOE Joint Genome Institute.
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/clone_lib="CalTech human BAC library C"
20745 a 22135 c 22612 g 21422 t
                                                                                                                                                                                                                                                                              AC011336.4 G1:9256274
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN
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100.0%; Pred. No. 0.00081;
ive 0; Mismatches 0;
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Db 38702 TCATGCATTACCACCCCCTCGGGACAGGCAG 38668
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Center clone name: CIT-HSPC_250113
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Center Code: JGI
Web site: http://www.jgi.doe.gov
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Best Local Similarity 100.(
Marches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
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JOURNAL
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Consensus quality: 78189 bases at least Q40

Consensus quality: 82001 bases at least Q30

Consensus quality: 82001 bases at least Q30

Consensus quality: 82001 bases at least Q30

Consensus quality: 83201 bases at least Q30

Consensus quality: 83201 bases at least Q30

Consensus quality: 83201 bases at least Q30

Estimated insert size: 83944; sum-of-contigs estimation

Quality coverage: 6.34 in Q30 bases; pulse field gel estimation

NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* on size of 7 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence will go f 2979 bp in length

* 3080 3476: contig of 24886 bp in length

* 59263 59362: gap of unknown length

* 59263 59362: gap of unknown length

* 76111 79613: contig of 16648 bp in length

* 76111 79613: contig of 16648 bp in length

* 76111 79613: contig of 16648 bp in length

* 76111 79613: contig of 16648 bp in length

* 76111 79613: contig of 16648 bp in length

* 76111 79613: contig of 16548 bp in length

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* 76111 79613: contig of 16548 bp in length

* 76111 79613: contig of 16548 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 84544)

DOE Joint Genome Institute.

Direct Submitsaion

Submitted (03-406-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:7454202.
                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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         Homo sapiens chromosome 5 clone XXpl-360D11, WORKING DRAFT SEQUENCE, 7 ordered pieces.
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Center clone name: XXp1-360D11

    .84544
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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Center Code: JGI
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Unpublished
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/clone="XXp1-360D11"
                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 84544)
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AC009012,3 GI:12830104
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TITLE

COMMENT

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Direct Submisted (03-AuG-1999) production Sequencing Facility, DOE Joint Submitted (03-AuG-1999) production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced 91:7708985.

-----Genome Center Center Center Contest of Secure 103 Method 10
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HOMO sapiens chromosome 5 clone CTB-113120, WORKING DRAFT SEQUENCE,
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                       gap of unknown length
contig of 8327 bp in length
gap of unknown length
gap of unknown length
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gap of unknown length
contig of 6611 bp in length
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gap of unknown length
contig of 16291 bp in length
gap of unknown length
contig of 15639 bp in length.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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39367 a 38414 c 39218 g 39915 t
                                                contig of 3551 by gap of unknown locontig of 7004 by gap of unknown locontig of 7004 by gap of unknown locontig of 5438 by gap of 15438 by gap
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Center Project Name: 107808, H233
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 142845 bases at least Q40
Consensus quality: 150910 bases at least Q30
Consensus quality: 150910 bases at least Q30
Consensus quality: 150756 bases at least Q30
Estimated insert size: 156920; sum-of-contigs estimation
Betimated insert size: 156920; sum-of-contigs estimation
Quality coverage: 8.41 in Q20 bases; pulse fleld gel estimation
Quality coverage: 8.42 in Q20 bases; pulse fleld gel estimation

* NOTE: This Is a "working draft' sequence. It currently
consists of 26 contigs. The true order of the places

* snot known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                   Direct Submission Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced gi:11178048.
                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 159420) Eob Joint Genome Institute. Sequencing of Human Chromosome 5 Unpublished
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Lontig of 1543 bp in length

Losting of 1543 bp in length

5629: contig of 2463 bp in length

5630 5729: gap of unknown length

730 6997: contig of 1268 bp in length

98 7097: gap of unknown length

98 9214: contig of 2117 bp in ''

11813: contig of 2117 bp in ''

11813: contig of

11813: contig of
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contig of 2356 bp in length
gap of unknown length
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unknown length
of 3487 bp in length
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of 4243 bp in length
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Center clone name: XXp1-929G6
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DOE Joint Genome Institute.
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                                         Consensus quality: 174733 bases at least Q40
Consensus quality: 186693 bases at least Q30
Consensus quality: 186693 bases at least Q30
Consensus quality: 190547 bases at least Q30
Consensus quality: 190547 bases at least Q30
Estimated insert size: 165000; pulse field gel estimation
Cuality coverage: 7.77 in Q20 bases; pulse field gel estimation
Quality coverage: 7.77 in Q20 bases; pulse field gel estimation
Quality coverage: 7.77 in Q20 bases; pulse field gel estimation

* NOTE: This is a "working draft' sequence. It currently

* consists of 29 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gapes are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                            1115: contig of 1115 bp in length
1215: gap of unknown length
2567: contig of 1352 bp in length
2667: gap of unknown length
3745: contig of 1078 bp in length
3845: gap of unknown length
4920: contig of 1075 bp in length
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

1 (Dases 1 to 1790)

Oosterwegel, M.A.

Direct Submission

Submitted (12-AUG-1991) M.A. Oosterwegel, Dept of Clin Immunol,

Univ Hospital Ulrecht, P.O. Box 85500, 3508 GA Ulrecht, THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1790)
Oosterwegel.M., van de Wetering,M., Dooijes,D., Klomp,L.,
Winoto,A., Georgopoulos,K., Meijlink,F. and Clevers,H.
Cloning of murine TCF-1, a T cell-specific transcription factor
interacting with functional motifs in the CD3-epsilon and T cell
Teceptor alpha enhancers
J. Exp. Med. 173 (5), 1133-1142 (1991)
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMTCSTF 1790 bp mRNA ROD 02-SEP-199 MGOSE mRNA for T-cell specific transcription factor. X61385 X61385.1 GI:54760 HMG box; T-cell specific transcription factor; transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product."T-cell specific transcription factor"
/protein_id="CAA43658.1"
/db_xref="G1:54761"
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                                                                                                                                                                                                                                                                  Length 200831;
                                                                                                                                                                    human BAC library B"
50695 t. 2823 others
9 137208: gap of unknown length
9 200831: contig of 63623 bp in length.
Location/Qualifiers
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100.0%; Pred. No. 0.00067;
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/db_xref="SWISS-PROT:Q00417"
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/note="ACT splice/exon M5"
761. 984
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="51"
/clone="crib-13120"
/clone=lib="CclTech human
a 46907 c 47140 g 50695
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/organism="Mus musculus"
/isolate="M2a/M5"
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/Lissue_type="thymus"
/cell_type="T cell"
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/codon_start=1
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* NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                              Quality coverage: 3.5 in Q20 bases; agarose-fp Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9513 10790: con...
10791 10890: gap of 10791 10890: contig of 4190 bp 1...
15081 15180: gap of 100 bp 1...
18824: contig of 3644 bp in length 100 bp 1...
aap of 100 bp 1...
18824: contig of 3645 bp in length 100 bp 1...
18925: contig of 3646 bp in length 100 bp 1...
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122442 122541: gap of 100 bp
122542 140243: contrg of 17702 bp in length
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140344 162496: contig of 22153 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97949: gap of 100 bp 109572: contig of 11623 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4362: gap of 100 bp
6417: contig of 2055 bp in length
16517: gap of 100 bp
9412: contig of 2895 bp in length
19512: gap of 100 bp
19512: gap of 100 bp
10790: contig of 1278 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52215: gap of 100 bp 55927: contig of 7712 bp in length 60027: gap of 100 bp 67115: contig of 7088 bp in length 67215: gap of 100 bp 75188: contig of 7973 bp in length
                                                                                                                                                                                                                                                                                                                                                                                1374 1473: gap of 1373 bp in length
1374 1473: gap of 100 bp
1474 2786: contig of 1313 bp in length
278 2886: gap of 100 bp
2887 2862: contig of 1376 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38881: gap of 100 bp
44764: contig of 5883 bp in length
4864: gap of 100 bp
52115: contig of 7251 bp in length
Consensus quality: 158956 bases at least 020
Insert size: 164000; agarose-fp
Insert size: 160296; sum-of-contigs
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1. .1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23229: gap of 100 bp 26859: contig of 3630 bp 26959: gap of 100 bp 32575: contig of 5616 bp
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109673 122441: contig of 12769 b
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2887. .4262
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/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cont 59927:
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97849: cont
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26860
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Unpub
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 11, clone RP23-46J7
                                                                                                                                                                                                                                                                                                                                                                                                                                             AC044846 162496 bp DNA HTG 22-JUL-2000
Mus musculus chromosome 11 clone RP23-46J7 map 11, WORKING DRAFT
SEQUENCE, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                    Length 1790;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                           1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: 46_J_7
------ Summary Statistics
Sequencing vector: M13, M77815; 100% of reads
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                    Score 28.6; DB
Pred. No. 0.56;
                                                                                                                                                                                                                                                                                               343 t
                                                                                                                                                                                                                                                               1 tcatgcattacccaccccctcgggagcagggcag 35
                                                                                                                                                                                                              0; Mismatches
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                                           436 g
                       /note="HMG-box"
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                                                                                                                                                       81.7%;
88.6%;
                                           587 c
                                                                                                                                                                                                              31; Conservative
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Best Local Similarity
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KEYWORDS
SOURCE
ORGANISM
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                                              BASE COUNT
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TITLE
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in length

100 bp f 5616 bp i

100 bp 6106 bp in length

contig of

p of 100 bp contig of 12108 bp in length

p of 100 bp contig of 10353 bp in length

gap of

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Hepatitis G virus
GBV-C/HGV group.
I (bases 1 to 318)
Sathar, M., Soni,P.N., Pegoraro,R., Simmonds,P., Smith,D.B.,
Dhillon,A.P. and Dusheiko,G.M.
A new variant of GB virus C/hepatitis G virus (GBV-C/HGV) from South Africa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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2 (bases 1 to 318)

2 (bases 1 to 318)

Sathar, M.A., Soni,P.N., Pegoraro,R., Simmonds,P., Smith,D.B.,
Dhillon,A.P. and Dusheiko,G.M.

Direct Submission
Submitted (27-JUL-1999) Medicine, University of Natal, Faculty of Medicine, Private Bag 7, Congella, Durban, Kwazulu Natal 4013,
Unpublished
2 (bases 1 to 318)
Sathar, M. Soni, P.N., Pegoraro, R., Simmonds, P., Smith, D.B.,
Dhillon, A.P. and Dusheiko, G.M.
Direct Submission
Submitted (27-JUL-1999) Medicine, University of Natal, Faculty of Medicine, Private Bag 7, Congella, Durban, KwaZulu Natal 4013,
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Hepailtis G virus isolate KZN-B23 5' untranslated region.
AF172535 GI:5802520
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88.5%; Pred. No. 5.8e+02;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                  Location/Qualifiers
Location/Qualifiers
Location/Qualifiers
Location/Qualifiers
/organism-"Hepatitis G virus"
/isolate="KxN-B20"
/db_xref="taxon:45255"
/country="South Africa"
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/db_xref="kaxon:45255"
/country="South Africa"
1, 318
/note="polyprotein"
a 99 c 105 9 5
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1. .318
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99 c 105 g
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Best Local Similarity 88.59
Matches 23; Conservative
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South Africa
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Hepatitis G virus
Viruses, SRNA positive-strand viruses, no DNA stage: Flaviviridae;
GBV-C/HGV group.
1 (bases 1 to 318)
Sathar.M.A., Soni,P.N., Pegoraro,R., Simmonds,P., Smith,D.B.,
Bhillon,A.P. and Dusheiko,G.M.
A new variant of GB virus C/hepatitis G Virus (GBV-C/HGV) from South Africa
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Hepatitis G virus isolate KZN-B20 5' untranslated region.
AF172532 GI:5802517
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SM Homo sapiens
Eutheria: Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria: Primates; Catarrhini; Hominidae; Homo.
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
Craigen, W.,
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Craigen, W.,
Mamm. Genome 10 (10), 1041-1042 (1999)
E 99431679
D 10501981
E 0 Chases 1 to 2321)
E 2 (bases 1 to 2321)
E 2 Chases 2 to 2321)
E Craigen, W.K., Bowles, K.R., Schatte, E.C., Towbin, J.A. and
Craigen, W.J.,
Craigen, W.K., Bowles, K.R., Schatte, E.C., Towbin, J.A. and
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                                                                HSVDAC2 2321 bp DNA PRI 19\text{-}O\text{CT}\text{-}1999 Homo sapiens voltage-dependent anion channel (VDAC1) gene, exons 2
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L Submitted (14-MAY-1999) Molecular and Human Genetics, Baylor

Submitted (14-MAY-1999) Molecular and Human Genetics, Baylor

College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Location/Cualifiers

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(Ab_Xref="Laxon:9606"

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                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                              Title:
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SUMMARIES			Description	Human gene express	Human ORFX ORF490	Human polynucleoti	Human polynucleoti	Clone related to F	Mouse IgH 3'-enhan	DNA encoding human	Human ataxia and r	Human colon cancer	Nucleic acid ligan	HIV-1 RT SELEX ide
			ID		AAC74935	AA160788	AA159002	AAV44840	AAQ31725	AAX04534	AAT61981	AAA02350	AAQ53563	AAT07727
	œ		DB	20	21	22	22	19	13	20	18	21	14	17
			e Match Length DB]	299	3500	3803	3804	512	1565	8210	8239	1704	4.1	41
		Query	Match	56.6	56.6	9.95	56.6	56.0	56.0	56.0	56.0	54.9	54.3	54.3
			Score	19.8	19.8	19.8	19.8	19.6	19.6	19.6	19.6	19.2	19	19
		i.t	No.		7	m	4	Ŋ	9	7	œ	Ġ,	10	11
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12	SELEX ligand 1.8 t Pseudoknot 1.8 of Random regiton 1.8 RNA ligand sequenc RNA ligand sequenc RNA ligand sequenc High-affinity nucl T. harzianum exoch CDNA encoding a he Nucleic acid seque Genomic fragment # Human genomic DNA Human polynucleoti Human polynucleoti	Probe #1305 for ge Probe #126 used t Probe #1279 used t Iluman bone marrow Arabidopsis thalia Human bone marrow Human genome from Human open clone (Human ORPX of F9126 Human NWDAR2 recep Angiotensin convertunan ORPX of F9126 Human N"methyl-D-a Human N"methyl-D-a Human N"methyl-D-a Human N"methyl-D-a Human N"methyl-D-a Human N"methyl-D-a	equence SEQ ID NO:1108.	diagnosis; therapy; probe; filing; forensic; cancer; reast cancer; lung cancer; ss.	Drmanac S; se K. Innis MA;
19 54.3 41 18 19 54.3 41 18 19 54.3 41 19 19 54.3 41 20 19 54.3 41 20 19 54.3 2000 18 19 54.3 2000 18 19 54.3 2000 20 19 54.3 2000 20 18 54.3 2000 20 18 53.7 11696 22 18.8 53.7 7661 22 18.8 53.7 7661 22 18.8 53.7 7661 22 18.8 53.7 11696 22 18.8 53.7 11696 22 18.8 53.7 11696 22 18.6 53.1 461 22 18.6 53.1 14793 22 18.6 53.1 14793 22 18.6 53.1 14793 22 18.4 52.6 1611 21 18.4 52.6 1611 21 18.4 52.6 1611 21 18.4 52.6 3050 22 18.4 52.6 4002 21 18.4 52.6 4002 22 18.4 52.6 3050 22 18.4 52.6 3050 22 18.4 52.6 3050 22 18.4 52.6 4002 21 18.4 52.6 9905 0006066 8.JAN-1998; 98US-0080666 8.JAN-1998; 98US-0080666 8.JAN-1998; 98US-0080515 1.MAR-1998; 98US-0080515 1.MAR-1998; 98US-0080515 1.MAR-1998; 98US-0080515 1.MAR-1998; 98US-0080515 1.MAR-1998; 98US-0080515 1.MAR-1998; 98US-0080515 1.MAR-1998; 98US-0080515 1.MAR-1998; 98US-0080515	AAVOOB12 AAV14619 AAV14697 AAV79694 AAV79672 AAA92772 AAA92772 AAA92794 AAA60261 AAA60261 AAA60261 AAA60261 AAA603983 AAA603983 AAA603983 AAA603983	AAI 1372 AAI 32640 AAI 32640 AAI 32640 AAI 8984 AAI 89871 AAI 89871 AAI 89871 AAI 89871 AAI 89871 AAI 89871 AAI 89871 AAI 89871 AAI 89871	BP. CDNA S	of of pr	nanac R
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19.00 Saper 1.00 Saper	; \rangle Residue \text{Residue \text{		standa 199 (:		98; 98; 98; 98; YSEQ YSEQ
				97 P P P P P P P P P P P P P P P P P P P	PR-1 PR-1 EB-1 AR-1 PR-1 PR-1 PR-1
	00000000000000000000000000000000000000	3 1 1 2 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3	SULT A1 A2 A2 A2 A1 12		4 O W W W O M

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                                                                                                                                                                                                                                                                                    The present invention describes a library of human polynucleotides

comprising the sequences given in AA212532 to AA21779 Also described is

comprising the sequences given in AA212532 to AA21779 Also described is

a method of detecting differentially expressed genes correlated with the

cancerous state of a mammalian cell, comprising detecting at least one

differentially expressed gene product in a test sample from a cell

collaboration of being ancerous, where the gene product is encoded by one

of the 5248 polynucleotide sequences given in AA212532 to AA217799. The

collaboration of polymorphisms believed to detection of expression levels,

mapping, tissue typing or profiling, forensics, genetic analysis and

detection of polymorphisms. Polypeptides encoded by the polynucleotides

can be used for ataing antibodies for experimental, diagnostic and

therapeutic purposes. The polynucleotides may also be used to construct

cherapeutic purposes. The polynucleotides may also be used to construct

arrays for diagnostics (which may be used to determine function of an

two cells (e.g. to identify abnormal or diseased tissue in a human, to

concells (e.g. to identify abnormal or diseased tissue in a human, to

diagnosis, prognosis and management of colorectal cancer, breast cancer,

can be alway and an adagement of colorectal cancer, breast cancer,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antlinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20; Length 299;
      Randazzo F, Reinhard C;
I, Williams LT;
                                                                                                                                                   Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORFX ORF490 polynucleotide sequence SEQ ID NO:979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 299 BP; 55 A; 99 C; 68 G; 62 T; 15 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.6%; Score 19.8; Ilarity 77.4%; Pred. No. 58; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 atgcattacccaccccctcgggagcagggc 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 ACGCAGTCACCTCCCCACTGGGGAGCAGGGC 97
               Lamson G, Leshkowitz D, Pot D, Ra:
Stache-Crain B, Sudduth-Klinger J,
                                                                                                                                                                                                                                              Claim 1; Page 914; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC74935 standard; cDNA; 3500 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC74935;
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; uninearly; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; cardiant; thrombolytic; coagulant; vasoiropic; antidabetic; hypotensive; dermaclogical; immunosuppressant; cardiant; thrombolytic; coagulant; vasoiropic; antidiabetic; hypotensive; dermaclogical; immunosuppressive; antidiabetic; hypotensive; dermaclogical; immunosuppressive; antidiabetic; hypotensive; dermaclogical; immunosuppressive; antidiabetic; hypotensive; or presence of or predisposition to, or preventing or Lreating cantidity and actions associated with an ORFX-associated disorder. The nucleic acids can be used for express ORFX proteins in gene therapy cactors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, by pretension, hypothyroidism, cholesterol ester storage, systemic lupus capternal or fungal infection, malaria, autoimmune disorders, asthma, barmaglobinuria, antiniflammatory disease, to cnhance contains, printiniflammatory disease, conhance conhance conhance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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77.4%; Pred. No. 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 957-959; 5507pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA160788 standard; cDNA; 3803 BP.
                                                                                                            02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
31-MAR-2000; 2000WO-US08621.
                                                                               99US-0127607.
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Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                     Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB40726
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                                                                               31-MAR-1999;
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymorleotides are useful of the invention may be used to treat diseases of the pripheral nervous containing a polypeptide or polymorleotide or system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, continisation of the activities such as Immune system suppression.

Cantininibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, ancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and contains and inflammation, leukaemias and contains and activity, arthritis and inflammation, leukaemias and contains an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3804 BP; 755 A; 1153 C; 1253 G; 643 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qian XB,
Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ma Y, (
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 56.6%; Score 19.8; D
I Similarity 77.4%; Pred. No. 69;
24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1205; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone related to FcR-IV coding sequence.
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                                                                                                                                                                                                                                                                                                    2000US-055317
2000US-055317
2000US-0598042.
2000US-06298042.
2000US-062912.
200US-0653450.
2000US-0653450.
2000US-0653450.
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P-PSDB; AAM39846.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                             WO200153312-A1.
                                                                                                                                                                                                                                                                                                                              25-APR 2000; 29-JUL-2000; 29-JUL-2000; 203-AUG-2000; 214-SEP-2000; 219-OCT-2000; 29-NOV-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification
                                                                    leukaemia; ss
                                                                                                                                                                                                                                                            26-DEC-2000;
                                                                                                                 Homo sapiens
                                                                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang J, V
Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rang YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV44840
TD AAV44
XX
AC AAV4
XX
DT 20-0
XX
DE Clon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities auch as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and CNNS disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ken F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 3803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3803 BP; 753 A; 1153 C; 1253 G; 644 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen R, Ma Y, (Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.6%; Score 19.8; D7.4%; Pred. No. 69; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4777; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 2055 ATGCTGTGCCCACTCCCCTCGGCACCCGGGC 2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 atgcattacccaccccctcgggagcagggc 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 1205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA159002/c
ID AA159002 standard; cDNA; 3804 BP.
                                                                                                                                                                                                                     21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-065191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                             26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.6'
Best Local Similarity 77.4'
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
Wang 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAM41632
                                                                                 WO200153312-A1.
                                  Homo sapiens.
                                                                                                                              26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT,
Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA159002;
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<u>:</u>

Ren F, Wa

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Gaps

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7;

Length 3804; Indels

91SE-0001740. 92WO-SE00375

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Mouse immunoglobulin H 3' enhancer - which cross-hybridises with rat 3' enhancer and is used to target tissue-specific gene
                                                                                                                                                                                                                                                (PETT/) PETTERSSON S.
                                                                                                                                                                                                                                                                                                                                        WPI; 1992-433660/52.
                                                                                                                                                                                                     07-JUN-1991;
                                                                                                                                                      03-JUN-1992;
                                                               W09221762-A.
                                                                                                           10-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                  expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX04534;
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AAX04534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a cDNA clone related to the DNA encoding the Fc receptor-like IV protein (FcR-IV) of the invention. Cells containing the BNA are used to express the recombinant protein, and to screen for specific (ant)agonists. The proteins are used to induce phagocytosis, and their (ant)agonists are used to treat immune complex related diseases (e.g. rheumatoid arthritis, systemic lupus erythematosus, heamolytic cancer, lymphoma, leukaemia, infection by intracellular pathogens etc). The antagonists are also useful as immunomodulators and inhibitors of viral (e.g. human immune deficiency or denque viruses) entry into cells. The proteins may also be used to screen for specific binding agents, i.e. (ant)agonists, for raising antibodies (Ab), and for identification of particular cells or tissues. The Ab can be used therapeutically as antagonists, as assay reagents for diagnostic determination of the levels of expression of the proteins and for affinity purification of the proteins. The DNA and its fragments are useful as hybridisation probes or primers for isolating related genes, in situ hybridisation (chromosome mapping) and diagnostically to measure mRNA expression.
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0
                     Fc receptor-like protein; phagocytosis inducer; rheumatoid arthritis; immune complex related disease; systemic lupus erythematosus; allerqy; haemolytic anaemia; thrombocytopaenia; anaphylaxis; cancer: lymphoma; leukaemia; infection; immunomodulator; viral entry inhibitor; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding Fc receptor-like polypeptides or their fragments - and related vectors, transformed cells and antibodies, useful for treating and diagnosing diseases of the haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 512 BP; 111 A; 121 C; 153 G; 102 T; 25 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; cross hybridisation; B cell specific; target; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 cctgcattcggtggcccctttgggagcagggcag 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catgcattacccaccccctcgggagcagggag 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.0%; Score 19.6; 73.5%; Pred. No. 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 38; Page 96-97; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ31725 standard; DNA; 1565
                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                 98WO-US01184.
                                                                                                                                                                                                                                                                                                                                          97US-0049872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse IgH 3'-enhancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-414105/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and immune systems
                                                                                                                                                                                                         WO9831806-A2
                                                                                                                                                                                                                                                                                                                                                                   21-JAN-1997;
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                 20-JAN-1998;
                                                                                                                                                                                                                                                                                                                                             .8-JUN-1997;
                                                                                                                                                                                                                                                     3-JUL-1998
                                                                                                                  FcR-IV; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ31725;
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Matches
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an Acci-bgli subfragment from the core of the rat 3'enhancer
an Acci-bgli subfragment from the core of the rat 3'enhancer
(nucleotides 437-748). Two overlapping gps. of clones (lambda M2 and
lambda M3) were isolated. Phage lambda M3 extends 3' of lambda M2.
The sequence of the mouse IgH 3' enhancer was determined and aligned
with that of the rat. Hybridisations of subclones of the mouse IgH
3' enhancer to phage lambda M2 showed that the 3' enhancers of mouse
and rat were present in the genome in opposite orientations. The
specific expression of genes, so may be used to target tissue
specific expression of proteins and in hybridoma technology. The
enhancer may be used to enhance expression of genes in host cells, in
transgenic animals. It may be used in the prodn. of monoclonal
cransgenic animals. See also AAQ31726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ataxia telangiectasia; ATM protein; assay; interaction; kinase activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1565 BP; 405 A; 388 C; 460 G; 312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19.6; DB 13;
Pred. No. 78;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 catgoattacccaccccctcgggagcagggcag 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX04534 standard; DNA; 8210 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding human ATR protein.
Claim 2; Fig 3A; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106..8040
/*tag= a
/product= ATR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.0%;
73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-APR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p53; screening; ATR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
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A cDNA clone (AAT61981) codes for human ataxia and rad related checkpoint protein (ATR) (AAW13152), which controls progression through the cell cycle. Probes based on the yeast homologue rad3 sequence (see also AAT61982) were used to amplify a fragment from human leucocyte cDNA, which was used to screen a macrophage library. The sequence was completed by RACE PCR. The gene has been localised to chromosome 3422-25. It may be involved in hereditary diseases such as cancer, chromosome breakage, unstable phenotype and repair damage sensitive phenotype. The ATR gene can be used in produce antisense molecules or dominant negative mutants. It can also be used to produce ATR protein and as a probe to detect ATR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human colon cancer cell line polynucleotide sequence SEQ ID NO:2341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous staic; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; cestrogen receptor-pesit cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 8239;
                                                                                                                                   Human ataxia and rad related checkpoint protein - and yeast homologue Rad3, controls progression through cell cycle and c screen for checkpoint mechanism abrogators, useful in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8239 BP; 2555 A; 1538 C; 1732 G; 2414 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escobedo J, Innis MA, Garcia PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 catgoattacccaccccctcgggagcagggcag 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 73.5%; Pred. No. 87;
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                            Claim 1; Page 39-41; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
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98US-0085537.
98US-0085696.
98US-0105234.
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(MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA e.g. in cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHIRON CURP. HYSEQ INC.
                                                                                WPI; 1997-192908/17.
                                                                                                  P-PSDB; AAW13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHIR ) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-1998;
                                                                                                                                                                                                         treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA02350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA02350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
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O
                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human ATR (FRP1) protein. The protein is used in the course of the invention. The specification describes an assay method for a compound able to modulate the interaction between ATM or a protein having an associated kinase activity and p53 or a protein having homologous phosphorylation sites. The assay comprises contacting a peptide fragment ATM with a relevant fragment of p53 and a test compound, and determining the interaction or binding between the substances and the test compound. The assay method is useful for screening for compounds able to modulate the interaction between ATM and p53. The screened agents, peptide fragments and mucleic acids are useful for therapy involving modulating ATM action e.g. in the treatment of cancer, immunosuppression or HIV infections by modulating phosphorylation of p53 by ATM, and for purifying the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                        Assay method for compounds modulating the interaction of ATM and p53 - useful for the treatment of e.g. cancer, immunosuppression and HIV infections and for the purification of the proteins ATM and ATR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ataxia and rad releated checkpoint protein; ATR gene; cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8210 BP; 2511 A; 1555 C; 1738 G; 2406 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ataxia and rad related checkpoint protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 56.0%; Score 19.6; DB 20; Best Local Similarity 73.5%; Pred. No. 87; Matches 25; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 catgoattacccaccccctcgggagcagggcag 35
                                                                                                                                 (CANC-) CANCER RES CAMPAIGN ȚECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 8b; 124pp; English.
                                                                                                                                                                          Smith GCM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT61981 standard; cDNA; 8239 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-GB02197
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                                                98GB-0015423
                                                                                         97GB-0014971
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                                                                                                                                                                          Lakin ND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; therapy; ss.
                                                                                                                                                                                                               WPI; 1999-073587/07.
                                                                                                                                                                                                                                     P-PSDB; AAW84271
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                                                    16-JUL-1998;
                                                                                         16-JUL-1997;
                                                                                                                                                                        Jackson SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATM and ATR.
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          27-JAN-1999
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Indels

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DNA polymerase; gp43; ligand; cell sorting; inhibitor; probe; HIV-1; systematic evolution of ligands by exponential enrichment; SELEX; bacteriophage coat protein; serine protease, mammalian receptor; mammalian hormone; mammalian growth factor; ribosomal protein; viral rev protein; reverse transcriptase; psuedoknot; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        target ligands comprises, contacting a candidate mixture with the target ligand so that nucleic acids with an increased affinity for the target can be partitioned from the remainder of the candidate mixture; partitioning the increased affinity nucleic acids from the remainder of the candidate mixture and amplifying them. Preferably this procedure is repeated numerous times to yield a desired level of ligand enrichment. A template DNA (AAO$2240) was used to synthesise candidate ligands (see AAO$22405 AAU$3557-053577) which are specific for HIV reverse transcriptase. This sequence
                                                                                        Stem 2(b) as does Stem 2(a) to 2(b)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A method (SELEX) for identifying nucleic acid ligands which bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying nucleic acids which bind target ligands \cdot by partitioning increased affinity nucleic acids from candidate mixt. and amplifying these nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%; Score 19; DB 14; Length 41 62.9%; Pred. No. 1.1e+02; Live 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41 BP; 13 A; 9 C; 13 G; 6 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 teatgeattacceaececectegggaggagggag 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV-1 RT SELEX identified ligand 1.8.
                                    m
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                                    Loop
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91US-0714131.
92US-0931473.
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                                                                                                                                                                                                                                             90US-0536428
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Matches 22; Conservative
25..29
/*tag= 1
/label= 1
30..33
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/label=
                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                         (UYRE-) UNIV RES CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-404920/50.
                                                                                                                                                                                                                                                                                                                                                                                             Tuerk C;
                                                                                                                                                                                                                                             11-JUN-1990;
                                                                                                                                                                                                                                                                                                   10-JUN-1991;
17-AUG-1992;
                                                                                                                                                                                                                                                                                   11-JUN-1990;
                                                                                                                                                                      US5270163-A.
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    stem_loop
                                                            stem_loop
                                                                                                                                                                                                                                                                                                                                                                                             Gold L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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                                                                                                                                                                                                                           invention also describes a method of detecting differentially expressed invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test cample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for centecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of cancer, or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptormer, and colon cancer.
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0
    Kennedy GC, Pot D, Kassam A;
R, Dickson M, Drmanac S, Labat 1;
Jones LW, Stache-Crain B;
                                                                                                                    Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ligand; identification; target; selection; amplification; partition; detection; binding; affinity; HIV; reverse transcriptase; human immunodeficiency virus; ss.
                                                                                                                                                                                                                   AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.9%; Score 19.2; DB 21; Length 1704;
80.8%; Pred. No. 1.1e+02;
iive 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1704 BP; 521 A; 396 C; 390 G; 21 T; 376 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid ligand for HIV reverse transcriptase.
                                                                                                                                                                              Claim 1; Page 927-928; 1097pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Randazzo F,
Crkvenjakov F
Garcia V, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stem 1(a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stem 1(b)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ53563 standard; RNA; 41 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 80.8
Matches 21; Conservative
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                                                  Leshkowitz D, Kita D,
              Giese K,
Drmanac R,
                                                                                    WPI; 2000-126369/11.
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                Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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Gaps

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Length 41;

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25-MAR-1998
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27-MAR-1995;
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25-MAR-1998
                                                                                                                            23-SEP-1997.
                                                                                                        JS5670637-A.
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                                                                                     Synthetic.
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                                                                                                                                                                                                                                    Gold L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
   AATO7716-T07740 represent HIV-1 reverse transcriptase (HIV-1 RT) ligands identified by a systematic evolution of ligands by exponential enrichment (SELEX) reaction. This sequence forms a pseudoknot structure carbinent (SELEX) reaction. This sequence for this SELEX reaction is represented by AATO7715. In a SELEX reaction, a target molecule is contacted with a mixture of random nucleic acids under conditions favourable for binding. Unbound nucleic acids are then separated from those bound to the target, and the nucleic acids are amplified to give a dissociated nucleic acids are amplified to give a ligand enriched mixture. These steps are repeated until the specific ligand enriched mixture. These steps are repeated until the specific contacted by acteriophage coat proteins, serine proteases, mammalian receptors, mammalian hormones, mammalian growth factors, ribosomal proteins, DNA polymerases and viral rev proteins. The ligands identified (such as this sequence) may be used in assays, diagnostic procedures, or cell sorting a sman unhibitor of the target molecule function. It may also be used as an inhibitor of the target molecule function.
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                                                                                                                                                    30.34
/*tag= f
/note= "stem 2(b) binds to stem 2(a) (bases 17-21)"
                                                                                _{\rm s}^{\rm c} stem 1(b) binds to stem 1(a) (bases 12-16)"
                                                                                                                                     e "stem 2(a) binds to stem 2(b) (bases 30-34)"
                                                       "stem 1(a) binds to stem 1(b) (bases 22-26)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                          Artificial nucleic acid ligands - for selected target proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.3%; Score 19; DB 17;
ilarity 62.9%; Pred. No. 1.1e+02;
Conservative 3; Mismatches 10
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     Location/Qualifiers
12..26
/*tag= a
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                                                                                                                                                                                                                                         90US-0536428
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900S-0536428
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                                       12..16
/*tag=
                                                                      22..26
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nes 22; Conserv
                                                                                                                                                                                                                                                                                                                 Gold L, Tuerk C;
                                                                                                                                                                                                                                                               10-JUN-1991;
11-JUN-1990;
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                                       misc_binding
                                                                       misc_binding
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                                                                                                                                                        misc_binding
                                                                                                                                                                                                 US5475096-A
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Best Local S
Matches 22
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                  stem_loop
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This sequence represents a nucleic acid ligand containing a pseudoknot motif which binds the human immunodeficiency virus type 1 (HTV-1) reverse transcriptase (RT). Ligands to the HTV-1 RT are isolated by the systematic evolution of ligands by exponential enrichment (SELEX) method of the invention. This method is especially used to isolate novel non-naturally occurring nucleic acid ligands having a specific binding affinity for a target molecule, where the target molecule is a protein and the nucleic acid ligand is not a nucleic acid known to bind the rarget molecule. The nucleic acid ligands can be used, e.g. in assay methods, diagnostic proceedures, cell ligands can be used, e.g. in assay methods, diagnostic proceedures, cell sorting, as inhibitors of target molecule function, as probes, as sequestering agents, for therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid ligands for binding proteins - obtained by systematic evolution of ligands by exponential enrichment procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Systematic evolution of ligands by exponential enrichment; SELEX; binding affinity; diagnosis; inhibitor; probe; catalyst; Lemplate; human immunodeficiency virus type 1; reverse transcriptase; ss.
                                                                 Systematic evolution of ligands by exponential enrichment; SELEX; binding affinity; diagnosis; inhibitor; probe; catalyst; template; human immunodeficiency virus type 1; reverse transcriptase; ss.
Pseudoknot motif SELEX ligand 1.8 to HIV-1 reverse transcriptase.
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Pred, No. 1.1e+02;
3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41 BP; 13 A; 9 C; 13 G; 6 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 teatgeattacceaccecetegggageagggag 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Column 57-58; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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62.9%;
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90US-0536428.
95US-0412110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 62.9
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-479527/44.
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WPI; 1998-041356/04
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                                                 than nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1990;
24-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5696249-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV14597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gold L,
Gold L,
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV14597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High affinity RNA ligand motif; polymer binding; cell sorting; inhibitor; systematic evolution of ligands by exponential enrichment; SELEX;
                                                                                                                                                                                                      This sequence represents a nucleic acid ligand which binds the human immunodeficiency virus type 1 (HIV-1) reverse transcriptase (RT). Ligands to the HIV-1 RT are isolated by the systematic evolution of ligands by exponential enrichment (SELEX) method of the invention. This method is especially used to isolate novel non-naturally occurring nucleic acid ligands having a specific binding affinity for a target molecule, where the target molecule is a protein and the nucleic acid ligand is not a nucleic acid known to bind the target molecule. The nucleic acid ligands can be used, e.g. in assay methods, diagnostic procedures, cell sorting, as inhibitors of target molecule function, as probes, as sequestering agents, for therapy or as catalysts.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                         Nucleic acid ligands for binding proteins - obtained by systematic evolution of ligands by exponential enrichment procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudoknot 1.8 of SELEX identified ligand for DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                               54.3%; Score 19; DB 18; Length 41; 62.9%; Pred, No. 1.1e+02; ive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                  Sequence 41 BP; 13 A; 9 C; 13 G; 6 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   1 teatgeattacceaececectegggageagggeag 35
                                                                                                                                                                                         Example 2; Column 55-56; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequestering agent; DNA polymerase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV14619 standard; RNA; 41 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           910S-0714131,
900S-0536428,
950S-0409442.
                                                      91US-0714131.
90US-0536428.
95US-0412110.
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                                   95US-0412110
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                                                                                               (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                      WPI; 1997-479527/44.
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t4.
                                                                                                                   Gold L, Tuerk C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage
                                                      10-JUN-1991;
11-JUN-1990;
27-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1990;
24-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5696249-A.
                                  27-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1997
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              23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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This sequence represents the pseudoknot portion of the random region of a ligand identified by a systematic evolution of liqands by exponential considered by a systematic evolution of liqands by exponential and independent (SELEX) reaction to isolate ligands specific for bacteriophage considerase. This sequence is part of a ligand of the invention. The ligands are non-naturally occurring nucleic acid the invention. The ligands are non-naturally occurring nucleic acid having the polynucleotide that binds to the ligand by anteson-Crick base pairing or triple helix binding; the ligand by anches a pairing or triple helix binding; the ligand by anches a molecule and the ligand is obtained by: (a) contacting the concern molecule with a candidate mixture of nucleic acids having the arget molecule with a candidate mixture of nucleic acids having the target molecule with a candidate mixture of nucleic acids having the target filinty for the target; and (c) amplifying the separated concerns a filinty for the target; and (c) amplifying the separated nucleic acids. Ligands as above that bind to natural or synthetic nucleic acids. Ligands as above that bind to natural or synthetic receptors, e.g. proteins, may be usoful in assays, diagnostic procedures or call sorting, as inhibitors of target molecule function, as probes, as sequestering agents, etc., or may have catalytic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                     Synthetic nucleic acid ligands - that bind to target molecules other
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Best Local Similarity 62.9%; Pred. No. 1.1e+02;
Matches 22; Conservative 3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41 BP; 13 A; 9 C; 13 G; 6 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 teatgeattacecacecectegggaggaggagg 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ucaaggauuaaccgacgccaacggggagaauggcag 35
                                                                                                                                                                                                      Example 1; Column 55-56; 137pp; English.
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90US-0536428.
95US-0409442.
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WPI; 1998-041356/04.
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Synthetic nucleic acid ligands – that bind to target molecules other
                                                than nucleic acids
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Example 1; Column 55-56; 137pp; English.

This sequence represents the random region of a ligand identified by a systematic evolution of ligands by exponential enrichment (SELEX) reaction to isolate ligands specific for bacteriophage TV DNA polymerase. This sequence is part of a ligand of the invention.

The ligands are non-naturally occurring nucleic acid ligand with specific binding affinity for a target molecule, where: the target molecule is not a polynucleotide that binds to the ligand by Matson-Crick base pairing or triple helix binding; the ligand by Matson-Crick base pairing or triple helix binding; the ligand by the target molecule, and the ligand is obtained by: (a) contacting the target molecule, and the ligand is obtained by: (a) contacting the target molecule with a candidate mixture of nucleic acids having the target. and (c) amplifying the nucleic acids having the highest affinity for the target; and (c) amplifying the separated nucleic acids. Ligands as above that bind to natural or synthetic nucleic acids. Ligands as above that bind to natural or synthetic polymers, cell surfaces, drugs, metabolites, cofactors, transition-state analogues or toxins, may be useful in assays, diagnostic procedures or connected as a solute and every metabolites, as probes, as a connected as a solute and every metabolites, and another and assays and an analogues or toxins, may be useful in assays, diagnostic procedures or connected and account of the page of target molecule function, as probes, as sequestering agents, etc., or may have catalytic activity.

Sequence 41 BP; 13 A; 9 C; 13 G; 6 U; 0 other;

; Gaps 0; Length 41; 10; Indels Ouery Match 54.3%; Score 19; DB 19; Best Local Similarity 62.9%; Pred. No. 1.1e+02; Matches 22; Conservative 3; Mismatches 10;

δλ qq

Search completed: February 20, 2002, 14:30:45 Job time: 12434 sec

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5, Appli 5, Appli 5, Appli 51, Appli 51, Appl 45, Appl 45, Appl 45, Appl 213, App 213, App 213, App 214, App 214, App

Sequence 2 Sequence 2 Sequence 2 Sequence 2

Sequence 5, Ap Sequence 5, Ap Sequence 51, A Sequence 51, A Sequence 51, A Sequence 51, A Sequence 45, A

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Johnson, Michael A.
APPLICANT: Trideaux, Christopher T.
APPLICANT: Prideaux, Christopher T.
TITLE OF INVENTION: Recombinant Avian Adenovirus Vector
TITLE OF INVENTION: Recombinant Avian Adenovirus Vector
FILE REFERENCE: 48-95a
CURRENT PAPLICATION NUMBER: US 08/448,617
EARLIER APPLICATION NUMBER: US 08/448,617
EARLIER APPLICATION NUMBER: US 09.08
EARLIER PILING DATE: 1994-04-14
EARLIER FILING DATE: 1994-04-14
EARLIER FILING DATE: 1993-04-14
EARLIER FILING DATE: 1993-04-14
NUMBER OF SEQ ID NOS: 8
SCHARE: PALENTING DATE: 1993-04-14
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APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONNENCE ADDRESS:
ADDRESSEB: Beaton & Swanson, P.C.
ATREET: 4582 South Ulster Street Parkway, #403
US-08-231-193A-5
US-08-486-273A-5
US-08-480-474-5
US-08-240-086A-5
US-08-241-193A-51
US-08-240-086A-51
US-08-480-474-51
US-08-480-474-51
US-08-480-474-51
US-08-940-086A-91
US-08-940-086A-45
US-08-940-086A-45
US-08-466-033-213
US-08-466-033-213
US-08-466-033-213
US-08-466-033-213
US-08-446-033-213
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US-08-444-733-213
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Pred. No. 32;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09272032A
Patent No. 6296852
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75.08;
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Best Local Similarity
Matches 24; Conserv
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              Denver
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CITY: De
STATE: C
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Sequence 72,
Sequence 94,
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Sequence 94,
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Sequence 7
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. cgn2_6/ptodata/2/ina/5A_COMB.seq:*

. cgn2_6/ptodata/2/ina/5B_COMB.seq:*

. cgn2_6/ptodata/2/ina/6A_COMB.seq:*

. cgn2_6/ptodata/2/ina/BE_COMB.seq:*

. cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

. cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

. cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WOTGPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: June 10, 1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .E: Beaton & Swanson, P.C.
4582 South Ulster Street Parkway, #403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.3%; Score 19; DB 1; 62.9%; Pred. No. 19; Live 3; Mismatches 10
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                                                                                                                                                                                 1 tcatgcattacccaccccctcgggagcagggcag 35
                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acid Ligands NUMBER OF SEQUENCES: 344 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 94, Application US/07714131C; Patent No. 5475096; Chustal, INFORMATION: APPLICANT: Larry Gold APPLICANT: Craig Tuerk
                                                                                                                                                                                                                                                                                                                    Squence 72, Application US/07714131C
Patent No. 547596
GENERAL INFORMATION:
APPLICANT: Craig Tuerk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
ATTORREY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NOMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                   Conservative
; TYPE: NUCLEIC ACID
; STRANDENRESS: single
TOPOLOGY:
US-07-931-4738-94
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STRANDEDNESS: sing
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Best Local Similarity
Matches 22; Conserva
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CITY: Denver
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US-07-714-131C-72
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US-07-714-131C-94
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US-07-714-131C-72
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                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/931,473B
FILING DATE: 19920817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANDRESSEE: Beaton & Swanson, P.C. STREET: 4582 South Ulster Street Parkway, #403 CITY: Denver STATE: Colorado STATE: Colorado IIP: 80237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/931,473B FILING DATE: 19920817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 94, Application US/07931473B Patent No. 5270163 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             FILING DATE: 1992/0817
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: BALTY J. SWANSON
REGISTATION UNMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFRAN: (303) 850-9900
TELEFRAN: (303) 850-901
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 nucleotides
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,215
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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CLASSIFICATION:
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US-07-931-473B-72
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US-07-931-473B-94
                  COUNTRY: U
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Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettee, 3.50 inch, 1.44 MG storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/412,110
FILING DATE: June 10, 1991
PRIOR APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION NUMBER: 07/556,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         1 UCAAGGAUUAACUGACGCCAACGGGAGAAUGGCAG 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 94, Application US/08412110
Sequence 94, Application US/08412110
Sequence 94, Application US/08412110
CENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 344
                                                                                                                                                                                                                                                                                                                        Score 19;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.3%; Score 19;
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                                                                             NEX01/C2
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: BAITY J. SWAIDSON
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NEXOL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 72:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: NE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (303) 793-333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ 1D NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        54.3%;
                                                                                                                                                                                        LENGTH: 41 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.99
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 41 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage COMPUTER: IBM compatible
                                                                                                                                                                        COMPUTER READSHLE FORM:

WEDDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/O7/714,131C

FILING DATE: June 10, 1991
                                                                 ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 tcatgcattacccaccccctcgggagcagggcag 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
           TITLE OF INVENTION: Nucleic Acid Ligands NUMBER OF SEQUENCES: 344 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,110
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               *** TELECOMUNICATION NUMBER: 33,215
**** TELECOMUNICATION INFORMATION: TELECOMUNICATION INFORMATION: TELEFAN: (303) 850-9901
*** INFORMATION FOR SEQ ID NO: 94: SEQUENCE CHARACTERISTICS: LENGTH: 41 nucleotides
TYPE: nucleic acid
STRANDEDNESS: Caid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
                                                                                                                                                                                                                                                                                                          FILING DATE: June 10, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: BATTY . SWANDSON
REGISTRATION NUMBER: 33, 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 62.9
Matches 22; Conservative
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                    CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                              80237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-714-131C-94
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DB 1; Length 41;
19;
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Pred. No. 19;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-noc
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage COMPUTER: IBM COMPLIBLE OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
'OUNTRY: USA
IP: ROYL
5: Swanson & Bratschun, L.L.C.
8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 72, Application US/08469609A
; Patent No. 5843653
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
ADDRESSED: Swanson & Bratschun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 tcatgcattacccaccccctcgggagcagggcag 35
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                             SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,442A
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXO1/C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ 1D NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 41 nucleotides
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Best Local Similarity 62.99
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                       Englewood Colorado
                                                                                  USA
                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                80111
    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-409-442A-94
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US-08-469-609A-72
                                                                                  COUNTRY:
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                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage COMPUTER: IBM compatible
                           10;
                                                                                                                                                                                                                                                                                                                                                               3: Swanson & Bratschun, L.L.C.
8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 tcatgcattacccaccccctcgggagcaggcag 35
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                                                                                        Best Local Similarity 62.9%; Pred. No. 19;
Matches 22; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/409,442A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXO1/C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-409-442A-94

Sequence 94, Application US/08409442A

Patent No. 5696249

GENERAL INFORMATION:
                                                                                                                                                                                                     Sequence 72, Application US/08409442A Patent No. 5696249 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 41 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  STREET: 8400 E.
CITY: Englewood
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                80111
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                                                                                                                                                                                  US-08-409-442A-72
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Swanson & Bratschun, L.L.C. STREET: 8400 E. Prentice Avenue, Suite 200 CITY: Englewood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.3%; Score 19; DB 62.9%; Pred. No. 19; Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 tcatgcattacccaccccctcgggagcagggcag 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,190
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR DATE:
PRIOR DATE:
PRIOR DATE:
PRIOR DATE:
JUNG DATE:
JUNG DATE:
JUNG DATE:
APPLICATION NUMBER:
RILING DATE:
PRIOR APPLICATION NUMBER:
RELING DATE:
APPLICATION NUMBER:
RELING DATE:
PRIOR APPLICATION NUMBER:
RELING DATE:
APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 72, Application US/09143190; Patent No. 6110900; GENERAL INFORMATION:
07/536,428
                                                                                REGISTRATION NUMBER: 33,215
REGISTRATION NUMBER: 33,215
RELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
INFORMATION FOR SEQ 1D NO: 94:
SEQUENCE CHARACTERISTICS:
                         FILING DATE: June 11, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                LENGTH: 41 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.3'
Best Local Similarity 62.9'
Matches 22; Conservative
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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US-08-469-609A-94
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage COMPUTER: IBM compatible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Swanson & Bratschun, L.L.C. STREET: 8400 E. Prentice Avenue, Suite 200 CITY: Englewood STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 2, Pred. No. 19; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 tcatgcattacccaccccctcgggagcagggcag 35
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Patent No. 5843653
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORPUTER: Law Compariture
OPERATING SYSTEM: MS-DOS
SOFTWARE: Worderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,609A
FILING DATE: June 6, 1995
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: MATCH 27, 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: MATCH 24, 1995
FILING DATE: UJUBE 10, 1991
APPLICATION NUMBER: 08/412,110
FILING DATE: MATCH 27, 1995
PRIOR APPLICATION DATA: 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: MATCH 24, 1995
PRIOR APPLICATION DATA: 1995
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA: 0.1991
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: BATCY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERNCE/CDOCKET NUMBER: NEXO1/C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-333
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 54.3%;
Best Local Similarity 62.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 41 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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US-08-469-609A-72
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US-08-469-609A-94
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Sequence 2, Application US/09103840A

Sequence 2, Application US/09103840A

Patent No. 6294328

GENERAL INFORMATION:
APPLICANT: FIRESCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCHICASIS
TITLE OF INVENTION: TUBERCHICASIS
TITLE OF INVENTION: 19867007.00
CURRENT PILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g US-09-103-840A-2
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: VERSER, John C.
TITLE OF INVENTION: TUBERCUIOSIS
TITLE OF INVENTION: TUBERCUIOSIS
TITLE REPERENCE: 2436-20007.00
CURRENT APPLICATION UNMABER: US/09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.1%; Score 18.6; DB 4; Length 4403765; 84.0%; Pred. No. 47; Live 0; Mismatches 4; Indels 0;
                                                                                                                                                                                  DB 3; Length 41;
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                                                                                                                                                                                                                                                                                                            1 teatgeattacecacecectegggageagggag 35
                                                                                                                                                                               54.3%; Score 19; DB
ilarity 62.9%; Pred. No. 19;
Conservative 3; Mismatches
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OTHER INFORMATION: H37Rv
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SEQ ID NO 1
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Best Local Similarity 84.03
Matches 21; Conservative
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   nucleic acid
                                                                linear
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Best Local Similarity
Matches 22, Conserva
TYPE: nucleic STRANDEDNESS:
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US-09-103-840A-2/c
          TYPE: UUCA:
STRANDEDNES;
TOPOLOGY:
US-09-143-190-94
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage COMPUTER: IBM COMPUTER: IBM COMPUTER: MS-DOS
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tcatgcattacccaccccctcgggagcagggcag 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         54.3%; Score 19; 62.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: WOTDPERFECT B.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,190
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REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
PRIOR A
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                                     TELEPHONE: (303) 793-333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 72: SEQUENCE CHARACTERISTICS: LENGTH: 41 nuclectides
TYPE: nucleic acid
STRANDEDNESS: single
             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (303) 793-333
TELEFAX: (303) 793-3433
INFORMATION FOR SEO ID NO: 94:
SEOUNCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Conservative
                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-09-143-190-72
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Best Local Similarity
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Gaps

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Ouery Match 53.1%; Score 18.6; DB 4; Length 4411529; Best Local Similarity 84.0%; Pred. No. 47; Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Search completed: February 20, 2002, 14:32:12 Job time: 14391 sec

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BB544489 BB544489
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AZ04966 GSSBru011
AZ04966 GSSBru011
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RC1-HT059
1024054G1
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I (bases 1 to 353)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Londact: Robert Strausberg, Ph.D.

Email: capabs refmail.nih.gov

Tissue Procurement: ATC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Cannortium (LLNL)

DNA Sequencing by: NIHI Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/L.NL at:

http://mage.llni.gov

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BB245996
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CM1-NT024
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BC383736 302052 MA
AW415192 49311 MAR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG386035 353 bp mRNA EST 12-MAR-2001
602455204F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583473 5',
                                                      HB381453 B
AQ480983 R
AQ471698 R
AW960157 E
BE177628 B
BC37298 1
AZ96214 E
BF407387 U
BF419958 U
BR419958 U
BG625362 F
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/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e: LicMi307 row: h column: 02 quality sequence stop: 276. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                             AL596682
BG025922
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99,150 Million cell updates/sec
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                                                                                                      February 20, 2002, 09:22:11; Search time 3793.25 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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    nucleic search, using sw model

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280
                                                                                                                                                                                                                      Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., Whi
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                                                                                                                                                                                                                                                                                                                                                                   Institute for Genomic Research
2 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                Medical Center Drive,
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/db_xref="ATCC (inhost):158998"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
                                                                                    /organism="Homo sapiens"
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                     ://www.tigr.org/tdb/hgi/hgi.html)
M13 Reverse.
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33; Conser
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1 (bases 1 to 40)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestell,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,J., Bennett,J., Cardenas, Schmitter,B., Ritter,E., Ronko,J., Bennett,J., Cardenas, Schmitter,B., Ritter,B., Ritter,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40UP from Gibco
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing
Washington University Genome Sequencing Center For information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrine Pancreas Consortium
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                      /note-"Organ: Pancreas; Vector: pzFrO-2; Site_1: Not1; Site_2: Xho1; Library constructed using Superscript plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Xho1 site destroyed during cloning. Size-selected by column fractionation; average insert size 1.2kb. Primary Library, unamplified."
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                                                                                                                                                                                                                                                                        /tissue_type="Total pancreas"
/dev_stage="Embryonic day 16.5"
/lab_host="TOP10"
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xhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Melton Mouse E16 5 Pancreas Library M1621"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="ICR"
                                                                                                                                                                                                                                                                                                                                                                                      /sex="Both"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI.) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                             BB584341 264 bp mRNA EST 30-NGV-2000 BB584341 RIKEN full-length enriched, adult male epididymis Mus musculus cDNA clone 9230105F22 5', mRNA sequence. BB584341 GI:11480885
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602904810F1 NIH_CGAP_Mam3
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High quality sequence stop: 647.
Location/Qualifiers
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30; Conser
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National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 649)
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Mus musculus
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                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                 /note-*Organ: mammary; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIH_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5034194"
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85.7%;
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
   72
                                                                       O
   . 6%;
   Score 25.4;
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p, unshiyama,y, Westover,A., Itoh,M., Nagaoka,S., Sasaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 264)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                     /note="Site_1: SalT; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9230105f22"
                                                                      3']. cDNA was cloned into the Xhol and RamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="epididymis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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DВ 10;

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Mammalia; Eutheria;
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plate: LLAM9950 row: j column: 08
High quality sequence stop: 684.
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Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
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/site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."

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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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26; Conservative
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                                                                                                       Email: scain@athersys.com
High quality sequence stop: 438.
Location/Qualifiers
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Fax: 216 361 9596
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                                                                                                                                                                                                                                                                                           Athersys, Inc.
                                                                                                                                                                                                                                                                                                             Contact: Scott J. Cain
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="fetal, 14 wk post-conception"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Lu31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2578406"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                         /organism-"Homo sapiens"
/db_xref="taxon:9606"
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78.8%;
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Pred. No. 5.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         (2001) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens cDNA,
                                                                                                                                                                                                                                                                     OH 44115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.5e+02;
7;
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SOURCE KEYWORDS VERSION

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RESULT 9
BF107882/c
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ORIGIN
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TITLE
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 teatgeattacceacccccctcgggagcagggc 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CLONA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM866 row: p column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF107882 934 bp
601823888R1 NIH_MGC_79
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 9
High quality sequence stop: 22.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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204 c 294 g 202 t 1 others
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/cell_line="HT1080"
                                                                                                                                                                      /note="Organ: placenta; Vector: pbNR-LIB (Cloutech);
/note="Organ: placenta; Vector: pbNR-LIB (Cloutech);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccgttatygcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACCGCCATTAYCGCC-3' and 3' adaptor
sequence: 5'-ATTCTAAAGGCCGAGCGGCCACATG-CT(3)) RN-3'
sequence: 5'-ATTCTAAAGGCCGAGCGGCCACATG-CT(3)) RN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:4043781"
/clone_lib="NIH_MGC_79"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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78.8%;
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60.6%;
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  Score 21.2; DB 11; Pred. No. 8.9e+02;
                                                                                                                      278 g
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                          Length 934;
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BF183334
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                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                 761 CAGGCAGCACTGAGCCCCCACTGGGGCAGGGCAG 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cdone is available royalty-free through LLNL;
INAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 1757 Std Error: 0.00
Seq primer: -400p from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                          mRNA sequence.
BF183334
                                                                                      601809422R1 NTH_MGC_18
Homo sapiens
                                EST
                                             BF183334.1 GI:11061534
                                                                                                       BF183334
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                                                                                                                                                                                                                                                                                                                              Double-Stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "a 273 c 222 g 214 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="TMAGE:2066580"
/clone_11b="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                           1718
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Pred. No. 8.9e+02;
0; Mismatches
                                                                                         Mismatches
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Best Local Similarity
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JOURNAL
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Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB066565
BB066565
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Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                      P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishik, Y., Ishikawa, J., Ishikawa, T., Ishikawa, T., Ishikawa, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigamoto, Y., Shiragawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaya, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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Plate: LLCM857 row: 1 column: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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/clone_lib="NMAGE:14040213"
/clone_lib="NIH_MGC_18"
/clone_lib="NIH_MGC_18"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7: Site_1: xhol; Site_2:
/note="Organ: lung; Vector: pOTB7: site_2: xhol; Site_2: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 bp mRNA EST 25-JUN-2000 RIKEN full-length enriched, 15 days embryo male testis Mus cDNA clone 8030453C20 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Eutheria; Primates; Catarrhini; Hominidae; Homo
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/db_xref="taxon:9606"
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76.5%;
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0; Mismatches
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Pred. No. 8.
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VERSION ACCESSION DEFINITION

AV047890.2 AV047890

Mus musculus cDNA clone

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COMMENT
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                                                 RESULT 1
AV047890
LOCUS
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Best Local
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Caroinci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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AV047890 329 bp mRNA EST
AV047890 Mus musculus adult C57BL/6J testis
1700071L01, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                   was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI" 71 c 49 g 114 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 185.0 Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="8030453C20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="testis"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
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                                                                                                                                                                                                                                                                                                           60.0%;
82.8%;
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                                                                                                                                                                                                                                                                                                           Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                              DB 10;
1e+03;
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SOURCE

ORGANISM

Mus musculus

EST. house mouse

KEYWORDS

REFERENCE

AUTHORS

COMMENT

TITLE JOURNAL

RIKEN Mouse ESTs Unpublished (1999)

Genome Science Laboratory Contact: Chie Owa

RIKEN 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Tel: 81-298-36-9145 Fax: 81-298-36-9098

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutharyota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 329)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akhira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, Akhira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Kawai, J., Kawai, J., Kojima, Y., Matsuyama, T., Niltsuma, H., Oda, H., Owa, C., Kikuchi, N., Kojima, Y., Matsuyama, T., Niltsuma, H., Oda, H., Owa, C., Sahok, S., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Okazaki, Y., and Hayashizaki, Y., Pyter Vancour Corrections of the state of t
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
(Proc. Natl. Acad. Sci. U.S.A. method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                      Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertca, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="170007LD1"
/clone_lib="Mus musculus adult C57BL/6J testis"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2001
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Best Local Similarity
Matches 24; Conserv
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                                                  Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al. 1999)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
1 (bases 1 to 247)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
Plate: 60 row: A column: 12
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Smith TPL
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21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai Ishii, Y., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Odd, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shiganoto, Y., Shiraki, T., Soqabe, Y., Sugahara, Y., Suzuki, H., Y., Shiganoto, Y., Shiraki, T., Soqabe, Y., Sugahara, Y., Suzuki, H., Y., Shiganoto, Y., Shiraki, T., Soqabe, Y., Sugahara, Y., Suzuki, H., Y., Shiganoto, Y., Shiraki, T., Soqabe, Y., Sugahara, Y., Suzuki, H., Y., Shiganoto, Y., 
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AV205089 RIKEN full-1
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               Email: genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 762 4366
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121 c 141 g 105 t
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/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
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/lab_host="DH10B"
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82.8%;
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le+03;
                                                                                                                                                                       Yokohama, Kanagawa 230-0045, Japan
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REFERENCE AUTHORS

TITLE

KEYWORDS SOURCE

EST

ORGANISM

Bos taurus

Bovidae; Bovinae;

Bos.

(bases 1 to 445)

VERSION

DEFINITION ACCESSION RESULT 14 BF606275/c

BF606275 445 bp mRN2 273269 MARC 3BOV Bos taurus BF606275 BF606275.1 GI:11706718

mRNA

cDNA 5', mRNA

FOCUS

В S

54 CATGCAAGACCCACCCACCGGGGAGCTG 2 catgcattacccacccccctcgggagcag 30

82

Matches Best Local

Similarity

60.0%;

Conservative

0;

Score 21; DB 10; Pred. No. 1e+03; 0; Mismatches 5

Indels

BASE COUNT ORIGIN

97

/tissue_type="testis" /dev_stage="adult" 92 c 79 g

61 t

FEATURES

Location/Qualifiers

source

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Search completed: February 20, 2002, 13:52:27 Job time: 16216 sec
                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
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                                                                                                     cal Similarity
25; Conserv
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
,Y.
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                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                               52
                                                                                                                                                                                                                                                                                                         /note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone=11D="RIKEN full-length enriched, adult male testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="testis"
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/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .247
                                                                                                                                                                                                      59.48;
78.18;
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Pred. No. 1.2e+03;
0; Mismatches 7;
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Perfect score:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 ccgccttcaatctgctcatgcattacc
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Gapop 10.0 , Gapext 1.0
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Listing first 45 s
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No.
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AUTHORS
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Z47361
                               Eukaryota; Metazoa; Chordata; Craniara; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases i to 1115)

Mayer,K.; Wolff,E., Clevers,H. and Ballhausen,W.G.

The human high mobility group (HMG)-box transcription factor TCF-1: novel isoforms due to alternative splicing and usage of a new exon
                                                                                                                                         Z47361.1 GI:619881 splice form D; T cell
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65.4 157677
59.4 165330
59.4 166063
59.4 175464
59.4 205347
58.9 10980
58.9 10980
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1151600
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AC011336
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AL138784
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AF54692B
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HSTCF1A
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HSTCF1C
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AC022786
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X61385 Mouse mkNA
AC044846 Mus muscu
AL138784 Human LNA
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AC022786 Homo sapi
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AC092067 Homo sapi
AC015481 Homo sapi
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X59869 Human TCF-1

X59870 Human TCF-1

X63901 Homo sapien

X59871 Human TCF-1

AC009012 Homo sapi

AC011336 Homo sapi

AC009017 Homo sapi

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AE005316 Escherich
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AC087233 Mus Muscu
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AP002887 Homo sapi
AL392111 Homo sapi
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SUMMARIES

REFERENCE AUTHORS

JOURNAL.

Unpublished
2 (bases 1

2 (bases 1 to 1115)
van de Wetering,M., Oosterwegel,M., Holstege,F., Dooyes,D.
suijkerbuijk,R., Geurts van Kessel,A. and Clevers,H.

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JOURNAL
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Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Submitted (40-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet, Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The human T cell transcription factor-1 gene. localization, and promoter characterization J. Biol. Chem. 267 (12), 8530-8536 (1992) 92235082
                                                                                                                                                                                                                                                      H. Sapiens TCF-1 mRNA for T ce 247362
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                                                                     1 (bases 1 to 1165)
Mayer,K., Wolff,E., Clevers,H. and Ballhausen,W.G.
The human high mobility group (HMG)-box transcription novel isoforms due to alternative splicing and usage G
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splice form E; T cell factor 1.
                                 Unpublished
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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               (bases 1 to 1165)
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de Wetering, M., Oosterwegel, M.,
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Pred. No. 0.00029;
Mismatches 0;
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Holstege, F., Dooyes, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-JAN-1995) Ballhausen W. G., Institut fuer
Humangenetik der Universitaet Erlangen-Nuernberg,
Schwabachanlage 10, Erlangen, Germany, D-91054
Location/Qualifiers
                                                                                                                                                                                                            HSTCF1A 1254 bp mRNA PRI 14-JUN-1991
Human TCF-1 mRNA for T cell factor 1 (splice form A).
X59869 X55327
X59869.1 GI:36785
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                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1254)
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Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht,
                                                                                                                                                 Homo sapiens
                                             Direct Submission
                                                               van de Wetering, M.
                                                                                                                                                                                         DNA-binding protein; HMG box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1165)
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91114695
See also x59869-x59871
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                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 2814)

van de Wetering,M.

Direct Submission
Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical Immunology, University Hospital, P.O. Box 85500, 3508 GA Utrecht, The Netherlands

2 (bases I to 2814)
                                                                                                                                                                                                                                                                                         Human TCF-1 mRNA for T cell factor 1 (splice form
van de Wetering,M., Oosterwegel,M., Dooijes,D. and Clevers,H. Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                     DNA-binding protein; HMG
                                                                                                                                                                                                                                                          x59870 x55329
x59870.1 GI:
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/note="HMG box"
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80. .8
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391 c 335 g
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Pred. No. 0.00029;
; Mismatches 0;
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35; Conserv
                                                                                                                                                                                l (bases 1 to 2855)
van de Wetering, M., Ossterwegel, M., Holstege, F., Dooyes, van de Wetering, M., Ossterwegel, A. and Clevers, H. Suijkerbuijk, R., Geurts van Kessel, A. and Clevers, H. The human T cell transcription factor 1 gene. Structure, localization, and promoter characterization J. Biol. Chem. 267 (12), 8530-8536 (1992)
   Van
                                                                                     Van de Wetering,M., Castrop,J., Korinek,V. and Clevers,H. Extensive alternative splicing and dual promoter usage generate Tcf-1 protein isoforms with differential transcription control
                                                                                                                                                                                                                                                                                       Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                               T-cell transcription factor; transcription
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                                                        properties Mol. Cell.
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92235082
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                   (bases 1 to 2855)
   de Wetering, M.L.
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                                                      Cell. Biol. 16 (3), 745-752 (1996)
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/note="HMG box"
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831 c 648 g 572
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Pred. No. 0.00028;
); Mismatches 0;
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1691. .1788,1843. .1890,2054. .2134)
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1691. .1798,1843. .1890,2054. .2134)
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/gene="TCF-1"
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                                        0;
                                      Score 35; DB
Pred. No. 0.0
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                                                      0.00028;
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                                           0;
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Human TCF-1 mRNA for T
x59871 x55328
x59871.1 GI:36789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 van de Wetering, M., Oosterwegel, M., Dooijes, D. and Clevers, H. Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box EMBO J. 10 (1), 123-132 (1991)
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Submitted (28-MAY-1991) M. Van De Wetering, Dept of Clinical Submitted, University Hospital, P.O. Box 85500, 3508 GA Utrecht, The Netherlands
                                                                                                                                                                                                         l Similarity
35; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             van de Wetering, M.
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                                                                                                                                                                                                                                                                                                                                              782
                                                                                                                                                                                                       100.0%; larity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/cell_line="Jurkat and HPB
/clone_lib="cDNA"
                                                                                                                                                                                                                                                                                                                                              /note="alternative splice site"
a 860 c 671 g 597 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGWSARDNYGKKKRRSREKHQESTTDPGSPKKCRARFGLNQQTDWCGPCR" 539. .769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Codon_start=1
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LSLYEHFNSPHPTPAAIPHPA IVPPSGKOELOPFDRNLKTQAESKAEKEAKKPTIKKPLNA
LMLGSGVPGHPAAIPHPA IVPPSGKOELOPFDRNLKTQAESKAEKEAKKPTIKKPLNA
FMLYMKEMHAKVIAECTIKESSAAINOILGRRWHALLSREEDOAKYPELAKKERQLIHMOLY
FMLYMKEMHAKVIAECTIKESSAAINOILGRRWHALLSREEDOAKYPELAKKERQLIHMOLY
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/gene="TCF-1"
                                                                                                                                                                                                                                                                                                                                                                                          /gene="TCF-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="HMG box"
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84544 bp
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Pred. No. 0.00028;
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       HTG
                                                                                                                                                                                                                                                        Length 2910;
       19-APR-2001
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                                                                            Query Match
Best Local
                                                     Matches
                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 78189 bases at least 040
Consensus quality: 82001 bases at least 030
Consensus quality: 82001 bases at least 020
Estimated insert size: 80000; pulse field qel estimation
Estimated insert size: 80000; pulse field qel estimation
Quality coverage: 6.34 in 020 bases; pulse field gel estimation
Quality coverage: 6.04 in 020 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* This sequence will be replaced

* This sequence will be replaced
1 ccgccttcaatctgctcatgcattacccacccccc 35
                                                                                                                                                                                                                                                                                                                                                                                 * by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 2980 3079: gap of unknown length

* 3080 34576: contig of 32979 bp in length

* 34677 59262: contig of 31497 bp in length

* 34677 59262: contig of 24586 bp in length

* 59263 59362: gap of unknown length

* 59263 59362: gap of unknown length

* 59363 76010: contig of 1648 bp in length

* 76111 79613: contig of 3503 bp in length

* 79614 79713: gap of unknown length

* 79614 79713: gap of unknown length

* 79714 80649: contig of 336 bp in length

* 80650 80749: gap of unknown length

* 80750 84544: contig of 3795 bp in length

* 80740: gap of unknown length

* 80750 84544: contig of 3795 bp in length
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1 (bases 1 to 84544)

DOE Joint Genome Institute.
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AC009012
AC009012.3 GI:12830104
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Center Project Name: 1189075, H71
Center clone name: XXp1-360D11
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Center Code:
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On Feb 14, 2001 this sequence version replaced 9i:7454202
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DOE Joint Genome Institute.
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                                                     35; Conserv
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                                                                                                                                                                                                             19558
                                                     Conservative
                                                                                                                                                                                                                                                             1. .84544
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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21740 c 22203 g 20376 t
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                                                                            100.0%;
                                                  Score 35; DB 2; I
Pred. No. 0.00027;
; Mismatches 0;
                                                                                                                                                                                                                667 others
                                                                                                        Length 84544;
                                                        Indels
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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AC011336/c
LOCUS
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Db 45292 CCCCCTTCAATCTCCTCATCCATTACCCACCCCC 45258
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                                                                                                                                                                                                                                            source
                                                                        Local
              1 ccgccttcaatctgctcatgcattacccacccccc 35
                                                                                                                                                                                                                                                                    Direct Submission
Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7710593.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN
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DOE Joint Genome Institute.
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AC011336
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                                                            35;
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Center clone name: CIT-HSPC_250113
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                                                         h 100.0%; Score 35; DB 2;
Similarity 100.0%; Pred. No. 0.00027;
35; Conservative 0; Mismatches 0;
                                                                                                                                                     20745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --Genome Center
                                                                                                                                                   /clone="CTC-250113"
/clone_lib="CalTech human BAC library C"
a 22135 c 22612 g 21422 t
                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                            Location/Qualifiers
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5 clone CTC-250113,
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                                                                                          Length 86914;
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WORKING DRAFT SEQUENCE,
                                                                 Indels
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RESULT 9
AC009017/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 142845 bases at least Q40
Consensus quality: 150910 bases at least Q20
Consensus quality: 150910 bases at least Q20
Consensus quality: 152756 bases at least Q20
Estimated insert size: 80000; pulse field gel estimation
Estimated insert size: 156920; sum-of-contigs estimation
Quality coverage: 8.41 in Q20 bases; pulse field gel estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

11023. Contin of 1423 be in length
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DOE Joint Genome Institute.
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AC008608
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35; Conservative (
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Center Project Name: 107808, H233
                                Project Information
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Consensus quality: 174733 bases at least Q40
Consensus quality: 186693 bases at least Q20
Consensus quality: 190547 bases at least Q20
Consensus quality: 190547 bases at least Q20
Estimated insert size: 1565000; pulse field gel estimation
Estimated insert size: 198031; sum-of-contigs estimation
Quality coverage: 7.77 in Q20 bases; pulse field gel estimation
Quality coverage: 6.47 in Q20 bases; pulse field gel estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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/tissue_type="thymus"
/cell_type="T cell"
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/isolate="M2a/M5"
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oosterwegel,M., van de Wetering,M., Dooijes,D., Klomp,L., Winoto,A., Georgopoulos,K., Meiljlink,F. and Clevers,H. Cloning of murine TCF-1. a T cell-specific transcription factor interacting with functional motifs in the CD3-epsilon and T cell
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/product="T-cell specific transcription factor"
/protein_id="CAAA3658.1"
/db_xref="GI:54761"
/db_xref="MGD:MGI:98507"
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AC044846/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RS Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barten, B., Linton, L., Nusbaum, C., Barten, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Barstlen, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Barstlen, V., Beda, F., Anderson, S., Baldwin, J., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Cooke, R., Janders, D., Ferreira, P., Fitzhugh, W., Gaqe, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grand-Pierre, N., Castle, S., Jones, C., Kann, L., Karalas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Looke, K., Madoonald, P., Marquis, N., McCertan, K., McPheeters, R., McCerthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Connell, P., O'Roil, D., O'Roil, D., O'Roil, D., O'Roil, D., Norman, C.H., O'Connor, T., O'Donnell, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vonna, G., Zainoun, J., Zimmer, A. and Zodv, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus chromosome 11 clone RP23-46J7 map 11, SEQUENCE, 23 unordered pieces. ACC044846
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 22, 2000 this sequence version replaced gi:7543812. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washigton.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus chromosome 11, clone RP23-46J7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 162496)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 162496)
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                                                                                                                                                                                   Center clone name: 46_J_7
                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
Chemistry: Dye-terminator Big Dye: 100% of roassembly program: Phrap; version 0.960731 Consensus quality: 149639 bases at least Q40 Consensus quality: 156386 bases at least Q30
                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                         Sequencing vector: M13; M77815;
                                                                                                                                                                                                                Center project name: L9174
                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="HMG-box"
1 587 c 436 g
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.1%;
                                                                                                                                                      Summary Statistics
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                             100% of reads
ye; 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 others
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misc_feature
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* 85642 85741: gap of 100 bp in length

* 85742 97849: contig of 12108 bp in length

* 97850 97949: gap of 100 bp

* 97950 109572: contig of 11623 bp in length

109573 109672: gap of 10620 bp

109673 122441: contig of 170 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52215; gap of 100 bp 59927; contig of 7712 bp in 159228 60027; contig of 7712 bp in 159928 60027; gap of 100 bp 67115; contig of 7088 bp in 169116 67215; gap of 100 bp 67216 7528; gap of 100 bp 75288; gap of 7973 bp in le 75289 85641. ~~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 158956 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109573 109672: gap of 100 bp
109673 122441: contig of 12769 bp in length
122442 122541: gap of 100 bp
122542 140243: contig of 17702 bp in length
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15081 15180: gap of 100 bp
15181 18824: contig of 3644 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18825 18924: gap of
18925 23129: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38782 38881: gap of 100 bp
44764: contig of 5883 bp in
48765 44864: gap of 100 bp
44765 52115: contig of 7251 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32576 32675: gap of 100 bp
32676 38781: contig of 6106 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23130 23229: gap of 100 bp
26859: countig of 3630 bp in
26860 26559: gap of 100 bp
26960 32575: contig of 5616 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40244 140343: gap of 100 bp
.40344 162496: contig of 22153 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18925 231.
23130 23229:
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1374 1473: gap of 100 bp
1474 2786: contig of 1313 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2787 2886: gap of 100 bp
2887 4262: contig of 1376 bp in length
4263 4362: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4263 4362:
                                      /note="assembly_fragment" 2887. .4262
                                                                                                               /note="assembly_fragment"
1474. 2786
/note="assembly_fragment"
                                                                                                                                                                                                                                                                              /clone="RP23-46J7"
                                                                                                                                                                                                                                                                                                                                                        /chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                   /clone_lib="RPC1-23 Female Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162496
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contig of 4205 bp in length
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f 7088 bp in length
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sum-of-contigs
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requests: clonerequestésager. ac. us, provingent l'active de manager. ac. us, provingent l'active de l'active d'active d'ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chrl
RP5-1102M4 is from the library RPGI-5 constructed by the group of
Pieter de Jong. Por further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pcyPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the entire insert of clone RP5-1102M4 The true left end of clone RP11-138J20 is at 140238 in this sequence. The true right end of clone RP11-401M16 is at 25073 in this sequence. The true right end of clone RP11-72P17 is at 92766 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7445. .7492.
/note="LiM3e repeat: matches -78. .-28 of consensus"
8876. .9427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluJb repeat: matches 163. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8876. .9427
/note="L2 repeat: matches 1837. .2451 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .133 of consensus"
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/clone_lib="RPC1.5"
1285. .1588
/note="AluSx repeat: matches 1. .304 of consensus"
36.7. .328
/note="AluY repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9685. 9886
/note="MER20 repeat: matches 1. .217 of consensus"
10646. .10959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluJo repeat: matches 1. .312 of consensus"
11591. .11731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .299 of consensus"
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UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .242 of consensus"
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/note="Alusx repeat: matches 1. .
6981. .7111
/note="FLAM_C repeat: matches 1.
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16815. .16935
/note="MiR repeat: matches 23. .1
17021. .17192
/note="AluSq/x repeat: matches 13
17193. .17500
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14747. .15040
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15236. 15371
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Human DNA sequence from clone RP5-1102M4 on chromosome 1, complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 150434)
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Submitted (08-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
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122542. .140243
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9513. .10790
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'note≂"assembly_fragment"
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20970. .2728/

// Anote="Alux repeat: matches 1. .297 of consensus"

27268. .27891

// Anote="Alux repeat: matches 4431. .4830 of consensus"

27696. .27838

// Anote="Alusg/x repeat: matches 133. .307 of consensus"

28175. .28848

// Anote="LiMi repeat: matches 5254. .5431 of consensus"

28174. .28655

// Anote="LiMi/D repeat: matches 2. .303 of consensus"

28674. .2873

// Anote="Alux repeat: matches 1. .299 of consensus"

29032. .2933

// Anote="Alux repeat: matches 1. .299 of consensus"

29176. .29674

// Anote="Alux repeat: matches 1. .297 of consensus"

29376. .29674

// Anote="Alux repeat: matches 1. .297 of consensus"

29376. .31037

// Anote="Alux repeat: matches 1. .297 of consensus"

20814. .30174
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// Acte="MIR repeat: matches 187. .261 of consensus" 23128. .23439 .23583
// Acte="Alubb repeat: matches 1. .302 of consensus" 23439. .23583
// Acte="MIR repeat: matches 32. .187 of consensus" 24747. .25037
// Acte="Alus repeat: matches 1. .302 of consensus" 25130. .25330
// Acte="Alus repeat: matches 1. .302 of consensus" 25138. .25633
// Acte="Alus repeat: matches 1. .299 of consensus" 25137. .26031
// Acte="Alus repeat: matches 2. .306 of consensus" 25137. .26031
// Acte="Alus repeat: matches 6. .273 of consensus" 26093. .26361
// Acte="Alus repeat: matches 6. .273 of consensus" 26152. .26671
// Acte="Alus repeat: matches 1. .296 of consensus" 26152. .26671
// Acte="Alus repeat: matches 1. .296 of consensus" 26157. .25068
// Acte="Alus repeat: matches 1. .296 of consensus" 26172. .26671
// Acte="Alus repeat: matches 1. .296 of consensus" 26172. .26671
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22355. .32355
/note="FRAM repeat: matches 1. .165 of consensus"
32646. .32960
                                                                                                                                         700te-"Multiple Tepeat: matches 1. .294 of consensus" 20503. 20713  
20503. 20713  
20560. 20339  
700te-"MBRSBA repeat: matches 4. .223 of consensus" 21056. 21339  
700te-"AluY repeat: matches 1. .285 of consensus" 21340. 21393  
700te-"B copies 3 mer taa 81% conserved" 21341. 21390  
710te-"25 copies 2 mer aa 74% conserved" 21395. 21697
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Anote-"Alusx repeat: matches 1. .307 of consensus"
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23050. .23127
                                           /note="MERIA repeat: matches 1. .522 of consensus" 19526. 19823
1076="Alusp repeat: matches 1. .296 of consensus" 19829. .20122
.173 of consensus"
/note="MIR repeat: matches 97.
18869. .19397
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 151349)
                                                                                                                                                                                                                                         Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humqueryésanger.ac.uk Clone requestres: clonerequest/Geanger.ac.uk
On Jan 22, 2001 this sequence version replaced gi:10039747.
                               /note="14 copies 2 mer ac 92% conserved"
34019, 34127
/note="L2 repeat: matches 2626, .2735 of consensus"
34129, .34128
/note="Auub repeat: matches 85. .299 of consensus"
35177, .35480
/note="Alusx repeat: matches 1, .304 of consensus"
35177, .3593, .35954
/note="Miss repeat: matches 59. .259 of consensus"
36163, .36228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome 1 clone RP5-1110L4 map q41-42.3, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
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42823. 43128
                                                                                                                                                                                   //note="Mir repeat: matches 73. .139 of consensus" 37036. .37376
//note="L2 repeat: matches 2079. .2503 of consensus" 37729. .37773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42823. .43128
/note="AluSx repeat: matches 1. .312 of consensus"
        consensus
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        repeat: matches 2295. .2369 of
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Pred. No. 14;
0; Mismatches 7;
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Center code: SC
Web site: http://www.sanger.ac.uk
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                           .33923
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80.0%;
        /note="L2
33896. .33
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Best Local Similarity 80.07
Matches 28; Conservative
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Direct Submission
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SOURCE
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Eutheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155332)
                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is another who won and their order in this sequence record is a rabitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Homo sapiens chromosome 1 clone RP11-72P17,
PRCARSES ***, in ordered pieces.
AL365439.9 GI:15020472
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/clone_lib="RPCI-5"
1. .22192
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fragment_chaln:1"
22293. .68699
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                                                  - Project Information
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                         Contact: humquery@sanger.ac.uk
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Direct Submission
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Submitted (18-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 25, 2001 this sequence version replaced gi:14970368.
                                                                                                                                                                                                                                                    Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 154754 bases at least Q40 Consensus quality: 154754 bases at least Q30 Consensus quality: 154919 bases at least Q20 Insert size: 15532; sum-of-contigs agarose-fp Quality coverage: 12.87x in Q20 bases; sum-of-contigs Quality coverage: 13.38x in Q20 bases; agarose-fp
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location Qualifiers
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80.0%; Pred, No. 14;
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a 39644 c 39869 g 36237
                                                                                                                                                                                                Search completed: February 20, 2002, 14:25:50 Job time: 14389 sec
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/db_xref="taxon:9606"
                                                                                                                                                      Center code: SC
Web site: http://www.sanger.ac.uk
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1. .155332
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/clone="RP11-72P17"
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Best Local Similarity
Matches 28; Conserva
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Human polynucleoti

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RESULT 1
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1 ccgccttcaatctgctcatgcattacccaccccc 35
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human 2F3 protein	Novel human polynu	Probe #7617 for ge	Probe #11304 used	Rat RISKMARKER2 CO	Nuclear mitotic ap	E6AP-binding prote	Human protein enco	Human breast and o	Human cREL nucleot	Human polynucleoti
SUMMARIES	ID	AAC84603	AAF64276	AA117684	AA142618	AAH22402	AAT77781	AAT78310	AAH99647	AAF21744	AA239581	AAI58345
		22	22	22	22	22	18	18	22	21	21	22
	Query Match Length DB	2797	418	525	525	650	1041	1092	1774	1786	2337	2457
ο¥	Query Match	57.1	54.9	54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3	54.3
	Score	20	19.2	19	19	19	19	19	19	19	19	19
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Human polynucleoti	John Como Comit	HUMBH HOMOLOGUE OF	purpher formula api	e program	N. meningitidis pa	Probe #22404 used	Human cDNA clone (Probe #9328 used t	Human cDNA sequenc	Human RNA metaboli	c glutamicum codin	c glutamicum codin	Human leptin gene	Human brain Expres	Human gene signatu	Human secreted pro	Aspergillus oryzae	Polynucleotide sed	rsosor		Tac	Ş.	Sequences of H. 1e	Mouse 22B/30B (can	Murine Lyst Long	Rhizobium species	Trum spec	secreted pr		CDNA		ORFX	Human clNNA sequenc	
	AAAU/84	AAA0783		AAT14301			AAH0945		AAU1715									AAX21230	AAD10144			AAX59851		AAT89255	AAT74199		AAV30459	AAC02284	AAV65326	AAH13490	AA139655			
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ALIGNMENTS

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Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                    S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF; CUL-1; cullin; CDC33; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax; Bad; Bc1-2; tumour; cytostatic; ds.
                                                                                                                                                                                                                                                                                  Kondo T;
BP.
                                                                    Human ZF3 protein encoding DNA.
AAC84603 standard; DNA; 2797
                                                                                                                                                                                                            05-JUN-2000; 2000WO-US15449.
                                                                                                                                                                                                                                    99US-0137494
                                            02-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                  Zhang H, Tsvetkov LM,
                                                                                                                                                                                                                                                                                                       WPI; 2001-061703/07.
P-PSDB; AAB48291.
                                                                                                                                                                                                                                                            (UYYA ) UNIV YALE.
                                                                                                                                                                WO200075184-A1.
                                                                                                                                                                                                                                     04-JUN-1999;
                                                                                                                                           Homo sapiens
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                         AAC84603;
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RESULT
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                                            The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SRP1), SRP2), SRP2-like proteins (ZF) and CUL-1 (a member of the cullin/ CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell SKP2 and SRP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innis MA, Garcia PD, Klinger J, Kässam A;
Kennedy GC, Pot D, Lamson G, Drmanac R;
Dickson M, Labat I, Leshkowitiz D;
LW, Strache-Crain B;
                                                                                                                                                                                                                                                                                                  Gaps
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Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iic; gene therapy; colon cancer; prostate cancer; lung cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the rolon prostate, comprises 3351 human polynucleotide sequences -
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                                                                                                                                                                                                                                                               Score 20; DB 22; Length 2797;
Pred. No. 52;
0; Mismatches 5; Indels (
                                                                                                                                                                                                                    Seguence 2797 BP; 807 A; 525 C; 582 G; 883 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polynucleotide, SEQ ID NO: 32.
                     Examples; Page 115-116; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kennedy GC,
                                                                                                                                                                                                                                                                                                                                                           183 TTCAATCTGCTCATGTTTTGAACTCC 156
                                                                                                                                                                                                                                                                                                                                      6 ttcaatctgctcatgcattacccacccc 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Paqe 549; 1046pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Randazzo F, Kenne
, Drmanac S, Dick
cia V, Jones LW,
                                                                                                                                                                                                                                                                      57.1%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF64276 standard; cDNA; 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0142310.
99US-0142311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US18374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                        23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-091805/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytostatic;
breast cancer; lung
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                        treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200102568-A2.
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Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2001
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Best Local Si
Matches 23;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #7617 for gene expression analysis in human cervical cell sample.
their gene products are used as genetic or biochemical markers (e.g. blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polymorleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
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analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                               Length 418;
                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                   Sequence 418 BP; 89 A; 93 C; 117 G; 114 T; 5 other;
                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                               8;
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                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                          79;
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                                                                                                                                                                                                                                                                                                                                                                                                                              218 CCTTCAATCTCCTAATCCACCCCCTACCCCC 187
                                                                                                                                                                                                                                                                                             Score 19.2;
Pred. No. 79
                                                                                                                                                                                                                                                                                                                                                                                                 4 cetteaatetgeteatgeattacceacecee 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
                                                                                                                                                                                                                                                                                                     54.9%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI17684 standard; DNA; 525
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                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                          Local Similarity
es 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04 - FEB - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
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                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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Screening hepatotoxic agent comprises contacting test cell population expressing RISKMARKER or INJURYMARKER with agent, comparing expression with reference population and identifying difference in expression
                                          Identification; toxic; hepatotoxic; differential gene expression;
NSAID; non-steroidal antiinflammatory drug; ds.
                        Rat RISKMARKER2 contig SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 9; 76pp; English
                                                                                                                                                                 22-NOV-1999; 99US-0166923.
18-FEB-2000; 2000US-0183531.
20-NOV-2000; 2000US-0717321.
                                                                                                                                            21-NOV-2000; 2000WO-US32049.
     22-AUG-2001 (first entry)
                                                                                                                                                                                                            (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                        WPI; 2001-355948/37.
                                                                                                                                                                                                                                   Gould-Rothberg BE,
                                                                                 Rattus norvegicus
                                                                                                    WO200138579-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                          31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT77781;
                                                                                                                                                                                                                                                                                                               levels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
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                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                               Probe #11304 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 525;
           ch 18. Score 19; DB 22; Length 525: 18. Similarity 81.5%; Pred. No. 99; 22; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                     Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 525 BP; 117 A; 134 C; 82 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.3%; Score 19; DB 22;
ilarity 81.5%; Pred. No. 99;
Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID No 11304; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513 CTGCCTTCAATCTGCTTATGATCTACC 487
                                                          1 cegeetteaatetgeteatgeattace 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                   26-MAY 2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0652366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH22402 standard; DNA; 650
                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                           2000US-0180312
                                                                                                                                     AAI42618 standard; DNA; 525
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                   genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488897/53
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es 22; Conserv
                          Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                             WO200157272-A2.
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
                                                                                                                                                                               17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH22402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                                                                                                           AA142618;
                  Query Match
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Matches
                                                                                                                  RESULT 4
AAI42618/C
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Gerwein RW;

Ramseh TM,

Dipippo VA,

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The present invention describes a method of screening a test agent for hepatotoxicity. The method comprises: (a) providing a test cell hepatotoxicity. The method comprises: (a) providing a test cell copulation comprising a cell capable of expressing one or more nucleic and sequences selected from the group consisting of RTSKMARKER 1-8 and INJURYMARKER 1-10; (b) contacting the test cell population with a catis sequences in the test cell population; (d) comparing the actis sequences in the test cell population; (d) comparing the expression of the nucleic acid sequence in an reference cell cappulation comprising at least one cell whose exposure status to a population comprising at least one cell whose exposure status to a population nevels of the RISKMARKER or INJURYMARKER sequences, if expression is the RISKMARKER or INJURYMARKER sequences. If expression is the RISKMARKER or INJURYMARKER sequences. If method is useful population and reference cell population.

The method is useful for identifying a hepatotoxic agent. The present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.3%; Score 19; DB 22; Length 650; illarity 71.4%; Pred. No. 1e+02; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIP-1; NIP-2; NuMA; nuclear mitotic apparatus; NuMA in cell division; proliferation; antibody; Ab; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear mitotic apparatus interacting protein, NIP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 650 BP; 131 A; 178 C; 217 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 cogecticaatetgeteatgeattaceceaecece 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT77781 standard; cDNA; 1041 BP
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Best Local Similarity
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06-JUN-1996;
                                               07-JUN-1995;
       19-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                      The sequences given in AAT7780.81 encode NIP-1 and NIP-2 (NIP = NUMA interfere mitotic apparatus) interacting protein). Compounds which interfere with the interaction of NUMA with a known NIP are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NUMA or NIP which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NUMA or NIP, it can be treated by admin. of the appropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cell differentiation; survival; carcinoma; psoriasis;
bidquitination; p53; tumour suppressor; homeostasis; papilloma virus;
epithelial cell; acne; icthyosis; aphthous ulcer; hair growth;
antibody; cell proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                           New nucleic acid encoding nuclear mitotic appts. interacting proteins – useful for modulating cell division and proliferation and in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1041 BP; 245 A; 311 C; 314 G; 171 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                              / Match 54.3%; Score 19; DB 18;
Local Similarity 71.4%; Pred. No. 1.1e+02;
Nos 25; Conservative 0; Mismatches 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= cln42
/note= "E6AP-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 ccgcctgccccacctcaggcatgtcccatcccc 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cogcottcaatctgctcatgcattacccaccccc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6AP-binding protein cln42 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..1092
                                                                                                                                                                                                                                        Claim 2; Page 64-65; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT78310 standard; cDNA; 1092 BP
                                                                                     96WO-US09504
                                                                                                         95US-0478408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                 McPherson SMG, Snyder MP;
     malignant cell growth; ss
                                                                                                                                                                     WPI; 1997-077270/07.
                                                                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                              (UYYA ) UNIV YALE.
                                                                                                                                                                               P-PSDB; AAW21730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                           Homo sapiens.
                                                                                      17-JUN-1996;
                                                                                                          17-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-0CT-1997
                                             WO9640917-A1
                                                                  19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT78310;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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The present sequence encodes the E6AP-binding protein cin42. E6AP mediates ubiquitination and so the inactivation of e.g. p53 tumour mediates ubiquitination and so the inactivation of e.g. p53 tumour call because the E6AP-binding protein is likely to be involved in normal cell homeostasis and in the pathogenesis of proliferative and cell homeostasis and in the pathogenesis of proliferation of gene expression or the differentiation disorders, e.g. regulation of gene expression or the coll surface receptors, biogenesis of rivolow by gene therapy, may useful in treatment and prevention of no papelloma virus infected transformed cells and carcinoma, and may also be used to regulate epithelial cell processes more generally, e.g. in be used to require epithelial cell processes more generally, e.g. in cases of psoriasis, acre, icthyosis, aphthous utcers it may also be used to generate antibodies which are used in immunossasys to be used to generate antibodies which are used in immunossasys to be used to generate antibodies which are used in immunossasys to combinant proteins and oligonucleotides useful as probes and primers for diagnostic detection of (mutant) mRNA for the protein in colling protein-encoding qenes, for the detection of mutations in E6AP-binding protein-encoding qenes, contact can be used to mis-expression of these genes or mis-incorporation of the protein in a mis-expression of these genes or mis-incorporation of the protein in a contact can be used to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGAP-binding proteins and related nucleic acid - useful modulating cell differentiation, survival etc., partic. treatment and diagnosis of carcinoma, psoriasis, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1092 BP; 260 A; 329 C; 324 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             risk of disorders characterised by cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein encoding cDNA sequence SEQ ID NO:482.
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                                                                                                                                                                                                                                                 Rolfe M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 66-68; 83pp; English.
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                                                                                                                                                                                                                                                 Beer-Romero PL, Draetta G,
96WO-US09040
                                                                                  95US-0484878
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                                                                                                                                                                                                                                                                                                                               WPI; 1997-087053/08.
P-PSDB; AAW23658.
                                                                                                                                                               (MITO-) MITOTIX INC.
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Best Local Similarity
Matches 25; Conserv
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Human breast and ovarian cancer associated antigen gene SEQ ID 131.
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             AAM AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
AAM25963. The proteins can have activities based on the tissues and
cells thys are expressed in, such as: antinframmatory; antirheumatic;
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
central nervous system; virucide; anti-HIV; fungicide; antimutagen;
cardiovascular; antianaemic; antiagregant; hemostatic; vulnerary;
cardiovascular; antianaemic; antiagregant; natiallergic; antiasthmatic;
antiparkinsonian; and immunostimulant. The proteins and polynucleotides
encoding them can be used in gene therapy, antisense therapy and vaccine
production, The proteins and polynucleotides are useful for screening for
agonists or antagonists of a protein and for the treatment and diagnosis
of disorders associated with the activity of a protein e.g. inflammation,
rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
infections, autoimmunity, genetic diseases, heamatopoietic disorders,
anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
costeoporosis, severe complained immunodeficiency, eczema, allergic
hinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
controlled and antered multiple sclerosis, depression,
controlled antered antered and antered and antered and antered and antered antered antered antered and antered and antered and antered and antered antered and antered and antered and antered antered antered antered and antered and antered and antered and antered and antered and antered antered and antered and antered antered antered antered and antered antered and antered antered antered antered antered antered and antered antered and antered and antered ant
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             cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%; Score 19; DB 22; 71.4%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 552-553; 1217pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                       23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                        22-DEC-2000; 2000WO-US35017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 54.39
Best Local Similarity 71.49
Matches 25; Conservative
                                                                                                           neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAM25706
                                                                                                                                                                                   WO200153455-A2.
                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                     26-JUL-2001
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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are esquences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the isolation and characterisation of the DNA and protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, proteins, autoimmune haemolytic aneamia, autoimmune thyroiditis, and allows.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                  nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes mellitus, Crohn's disease, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 1786 BP; 453 A; 541 C; 476 G; 316 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 579; 1299pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 71.43
Matches 25; Conservative
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P-PSDB; AAB58841.
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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(HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                            14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                        25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                   26-DEC-2000;
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                                                                                                              21-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides antisense compounds targeted to a coding region, 3'UTR or 5'UTR of a nucleic acid molecule encoding human CREL (transcriptional activator). The antisense compounds are useful as research agents and diagnostics such as in the elucidation of the function of a particular gene. The antisense compounds can be useful as therepeutic modalities that can be configured to be useful in treatment regimes for treatment of cells, tissues and animals, especially humans. In the prior art, there are no known therapeutic agents which effectively inhibit the synthesis of cREL and additional agents capable of inhibiting cREL function are still required. The present sequence represent the human CREL sequence (GenBank Acon No: X75042).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 21; Length 2337; pred. No. 1.3e+02; 0; Mismatches 10; Indels
                                                                                                                           Human; CREL; transcriptional activator; antisense compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2337 BP; 722 A; 491 C; 524 G; 598 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense modulation of human CREL expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 13; Column 31; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polynucleotide SEQ ID NO 548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF;
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                                                                          Human cREL nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker
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Best Local Similarity 71.4%;
Matches 25; Conservative
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            28-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-061889/05
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                                                                                                                                                                     SS.
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                                                                                                                                                                     therapeutic;
                                                                                                                                                                                                                            Homo sapiens.
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, in munosuppressant and cytostatic acitvity. The polymorlectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous containing a polypeptide or polymuclectide of system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic collication of the activities such as: Immune system suppression, utilisation of the activities such as: Immune system suppression, and homolytic activity, chemotactic/chemokinetic activity, heamostalic assays for receptor activity, arthritis and inflammation, leukaemias and constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                            Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                      Ren F, Wang J;
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                                                                                                                                                                                                                                                                                                                                                                                         Qian XB,
Yang Y,
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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                                                       2000US-0488725.
2000US-0552317.
2000US-0528042.
2000US-0653450.
2000US-0653450.
2000US-0653450.
2000US-0653450.
2000WO-US34263.
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P-PSDB; AAM39189.
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Best Local Similarity
Matches 25; Conserv
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Wang Z, W
Zhou P,
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Homo sapiens
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat disease of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system as peripheral nervous injuries, peripheral nervous system and repressed and central nervous system diseases, such as lateral as peripheral sease, municipation of alsease, such as intilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constructions.
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                                                                                                                                                                                                                                                                                           Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating disorders
                                                                                                                                                                                                                                                                                             Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of (Hs-UNC-53/1) fragment from BAC 585 \pm 09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2548;
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                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
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Matches 25; Conservative 0; Mismatche.
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 4120; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, us
such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA07842 standard; cDNA; 4984 BP
                                                                                                                                                                                                                                                                                                Asundi V,
Wehrman T,
                                                                                                                                                                         2000US-0620312.
2000US-0653450.
2000US-0662191.
                                                                                                                                                                                                                     19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                               2000US-0552317.
2000US-0598042.
                                                                                                 26-DEC-2000; 2000WO-US34263
                                                                                                                                2000US-0488725
                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                  Liu C, A
Wang 2, W
Zhou P,
                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAM40975
                                          WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification
                                                                                                                                               25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUL-2000
                                                                                                                                                                                           03-AUG-2000;
                                                                                                                                                                                                          14-SEP-2000;
             Homo sapiens.
                                                                                                                                  21-JAN-2000;
                                                                       26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA07842;
                                                                                                                                                                                                                                                                                                                    Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                   rang YT,
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AAA07842
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The invention provides vertebrate (human) protein homologue of a UNC-53 crop rotein of Caenorhabditis elegans. The UNC-53 binds to microtubules or their plus ends. The UNC-53 sequences are used to promote neutal control of caenoration, revascularization and wound healing; also for treating reqenerative disease, acute traumatic injury, fibrotic disease and neurodegenerative diseases (e.g. rheumatoid arthritis and sclerosis). The autoimmune diseases (e.g. rheumatoid arthritis and sclerosis). The proteins, as a source of probes for detecting allelic variants and proteins, and as source of probes for detecting allelic variants and proteins and as source of therapeutic antisense sequences. Cells the expression; and as source of therapeutic antisense sequences. Cells the expression and as source of therapeutic antisense sequences. Cells that expression are used to identify regulators of cell shape, express the protein are used to identify regulators of cell shape, concerns that are involved in signal transduction pathways also involving the compounds that alter attechment of UNC-53 to used to deliver the target gene coupled to a UNC-53 encoding sequence may be concerned by the present sequence represents the nucleotide sequence of a 4984 consorted from RAC 585E09 (contains a putative 5' exon sequence of a 4984 consorted to a UNC-53/1) extending the sequence derived from cDNA libraries shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel proteins and nucleic acids e.g. for treating neurodegeneration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human homologue of UNC-53 (Hs-UNC-53/1) nucleotide sequence.
                                                                                                                                                                                                                                                                                                                             Bogaert TAOE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4984 BP; 974 A; 1475 C; 1579 G; 956 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    De Raeymaeker MC, Geysen JJGH,
Verhasselt P, Van De Craen M;
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2873..3043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1G; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA07835 standard; cDNA; 6004 BP.
                                                                                                                            99WO-EP03848
                                                                                                                                                                                                98GB-0011962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.39
Best Local Similarity 71.49
Matches 25; Conservative
                                                                                                                                                                                                                                                                            (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-116370/10.
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misc_feature
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                                                                                                                                    02-JUN-1999;
                                                                                                                                                                                                        03-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                   Luyten WHML,
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W09963080-A1
                                                                   09-DEC-1999
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/*tag= a
/note= "all C's are 2'NH2 cytosine, and all U's are 2'NH2
uracil"
 Immunoglobulin E; RNA ligand; inhibitor; IgE receptor; therapy; asthma; IgE dependent reaction; allergic disease; allergic rhinitis; hay fever; atopic dermatitis; chronic skin irritation; anaphylactic shock; IgE; ss.
                                                                                                                                                                                                                                                                                                                                                                               Identification of high-affinity IgE oligo:nucleotide ligands - which inhibit interaction of IgE with its receptor, which are therefore useful in diagnostic and therapeutic applications
                                                                                     Location/Qualifiers
1..91
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 39; 88pp; English.
                                                                                                                                                                                                                                                                                                                                  Tasset D, Wiegand TW;
                                                                                                                                                                                                                                95WO-US12401.
                                                                                                                                                                                                                                                           95US-0471985.
94US-0317403.
                                                                                                                                                                                                                                                                                                      (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-209316/21
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                                                                                                         modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 23;
                                                                                                                                                                                                                                                                             03-OCT-1994;
                                                                                                                                                                             WO9610576-A1
                                                                                                                                                                                                                                  27-SEP-1995;
                                                                                                                                                                                                                                                              06-JUN-1995;
                                                                                                                                                                                                        11-APR-1996.
                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides vertebrate (human) protein homoloque of a UNC-53 protein of Caenorhabditis elegans. The UNC-53 binds to microtubules or their plus ends. The UNC-53 sequences are used to promote neural regeneration, revascularization and wound healing; also for treating neurodegenerative disease, acute traumatic injury, fibrotic disease and autorimente diseases (e.g. rheumatoid arthritis and sclerosis). The UNC-53 polynucleotides can be used for recombinant production of the proteins, as a source of probes for detecting allelic variants and polymorphisms, for sequencing genomic DNa and for detecting UNC-53 expression; and as source of therapeutic antisense sequences. Cells that express the protein are used to identify regulators of cell shape, growth, motility and migration. They can also be used to identify proteins that are involved in signal transduction pathways also involving UNC-53, and to identify compounds that alter attachment of UNC-53 to microtubules. Carget gene coupled to a UNC-53 encoding sequence may be used to deliver the target gene to a cellular microtubule or its plus ends. The present the uncertain are sequence of the first human homologue
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                                                                                                                                                                                                                                                                                                                                                                                                           Novel proteins and nucleic acids e.g. for treating neurodegeneration
                                    3098..3121
/*tag= b
/*tag= b
/note= "this region is found to be absent in a
variant cDNA isolated from frontal cortex"
    /*tag= a
/note= "this region is found to be absent in a
variant cDNA isolated from frontal cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.3%; Score 19; DB 21; Length 6004; 71.4%; Pred. No. 1.5e+02; tive 0; Mismatches 10; Indels (
                                                                                                                  /*tag= c
/note= "this region is found to be absent in
variant cDNA from Hela or colorectal
                                                                                                                                                                                                                                                                                                                         Bogaert TAOE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6004 BP; 1470 A; 1844 C; 1562 G; 1127 T; 1 other;
                                                                                                                                                                                                                                                                                                                        De Raeymaeker MC, Geysen JJGH,
Verhasselt P, Van De Craen M;
                                                                                                                                                         adenocarcinoma tissue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ccgccttcaatctgctcatgcattacccaccccc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of UNC-53, designated Hs-UNC-53/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 92; Fig la; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IgE binding ligand IGEL 47.1.
                                                                                                                                                                                                                                                                      98GB-0011962.
                                                                                                                                                                                                                                         99WO-EP03848
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ID AAT14299 standard; RNA; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.45
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                 (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                     2000-116370/10.
                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY85564
                                                                                                                                                                                      409963080-A1.
                                                                                                                                                                                                                                                                                                                            Luyten WHML,
Maerten LJS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-1996
                                                                                                                                                                                                                                           02-JUN-1999;
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                                                misc_feature
                                                                                                     misc_feature
                                                                                                                                                                                                                09-DEC-1999
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AAT A280-T14320 represent RNA ligands for immunoglobulin E (19E). These sequences are non-naturally occurring RNA ligands, and were isolated and sequences are non-naturally occurring RNA ligands, and were isolated and sequences of purified using the method of the invention. In this method, a candidate mixture of nucleic acids is prepared, and contacted with IgE. The mixture are sequences with an increased affinity to 19E relative to the mixture are partitioned off from the rest of the mixture. The partitioned sequences are then amplified, to yield a mixture of nucleic acids enriched for those with relatively higher affinity and specificity for 1gE binding. The method can be repeated in order to obtain a mixture of higher specificity for 1gE binding. This method can be carried out with higher specificity for 1gE binding. This method can be carried out with higher specification for the 19E ligands inhibit the function of 1gE by preventing the 19E/receptor interaction. The 1igands are therefore useful in diagnostic and therapeutic applications for diseases associated with 1gE dependent reactions. The 19E dependent reactions include allergic diseases such as allergic rhinitis (hay fever), asthma, and anaphylactic shock.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
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Job time: 12450 sec
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Sequence 1, Appli
Sequence 2, Appli
Sequence 18, Appl
Sequence 136, Appl
Sequence 136, Appl
Sequence 136, Appl
Sequence 137, Appl
Sequence 137, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 93, Appli
Sequence 93, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 2337;
30;
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Monia.

APPLICANT: Monia. Brett P.

APPLICANT: Baker., Brenda F.

APPLICANT: Cowsort., Lex M.

TITLE OF INVENTION: Antisense Modulation of CREL Expression
FILE REPERENCE: RTS-0010
CURRENT APPLICATION NUMBER: US/09/156,253C
CURRENT APPLICATION NUMBER: 1998-09-18
NUMBER OF SEQ 1D NOS: 48
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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105-08317-403A-26/C
105-08317-403A
Sequence 26, Application US/08317403A
Sequence 26, Application US/08317403A
Sequence 26, Application US/08317403A
Tatent No. 5629155
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO IMMUNOGLOBIN E
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, I.L.C.
STREET: 8400 East Prentice Avenue, Suite 200
  US-08-875-972-1
US-07-808-455A-2
US-08-888-077A-118
US-08-967-101-136
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US-08-855-146-2
US-08-855-146-3
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US-08-823-110-3
US-08-823-110-3
US-08-933-75-05-93
US-09-933-75-05-93
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                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09156253C Patent No. 6001652 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.3
Best Local Similarity 71.4
Matches 25; Conservative
        1417 2
2229 1
2226 2
2276 2
2285 2
2285 2
2285 2
2285 3
3321 4
3321 4
3321 4
3333 3
3433 3
3433 3
4403765
1572
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ORGANISM: Homo sapiens
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STREET: 8400 East
CITY: Englewood
           550.3
500.3
500.3
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500.3
500.3
644
649.7
7
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US-09-156-253-1
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Sequence 26, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 46, Appli
Sequence 46, Appli
Sequence 46, Appli
Sequence 46, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
                                                                                                       February 20, 2002, 14:32:27 ; Search time 162.84 Seconds (without alignments) 48.678 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_NA:*

.cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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.cgn2_6/ptodata/2/ina/6B_COMB.seq:*

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Compugen Ltd.
                                                                                                                                                                                      ecgeetteaatetgeteatgeattacecaceecc 35
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US-08-317-403A-26

US-08-471-985A-26

US-08-471-985A-28

PCT-US95-12401A-28

PCT-US95-12401A-28

PCT-US95-12401A-28

PCT-US95-13536-2

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US-09-157-17

US-09-157-10-3

US-08-915-13536-1

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US-08-915-135-1

US-08-915-135-5

US-08-936-135-5

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US-08-946-63

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US-09-283-011-1
US-09-016-000-7
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                                                                                                                                                                                                                                                     351203 seqs, 113238999 residues
                                                                                                                                                       US-09-904-420A-1_COPY_851_885
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                                 GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                           Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match Length
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Perfect score:
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WIEGAND, TOTSLEN Walter
APPLICANT: GOLD, Larry
APPLICANT: TASSET, Diament
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: IMMUNOSLOBIN E
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Swanson & Bratschun, L.L.C. STREET: 8400 East Prentice Avenue, Suite 200 CITY: Englewood
                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: All U's are 2'-NH2 uracil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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76.7%; Pred. No. 19;
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COMPUTER: IBM compatible
OPERATING SYSTEM: WAS JOS
SOCIETE: WordDerfect 6.0
CURSETH APPLICATION NUMBER: US/U8/471,985A
FILING DATE: 06-JUNE-1995
CLASSIFICATION NUMBER: 08/317,403
FILING DATE: 03-OCTOBER-1994
PRIOR APPLICATION DATE: 10-JUNE-1991
FILING DATE: 10-JUNE-1991
FILING DATE: 10-JUNE-1991
FILING DATE: 11-JUNE-1991
FILING DATE: 11-JUNE-1991
FILING DATE: 11-JUNE-1991
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-471-985A-26/c; Sequence 26, Application US/08471985A; Patent No. 5686592; GENERAL INFORMATION:
                                                                                                                                NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX23
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 91
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Best Local Similarity 76.7
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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                                                                                  MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,403A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T., GOLD, L., AND TASSET, D. HIGH-AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               All C's are 2'-NH2 cytosine
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STREET: 8400 East Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
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TO IMMUNOGLOBIN E
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76.7%; Pred. No. 19;
:ive 0; Mismatches
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SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,403A
FILING DATE: 3-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                   Sequence 28, Application US/08317403A
Patent No. 5629153
GENERALINFORMATION:
APPLICANT: WIEGAND, T., GOLD, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.7%
Best Local Similarity 76.7%
Matches 23; Conservative
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TITLE OF INVENTION: OLIC
TITLE OF INVENTION: TO 1
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                        Colorado
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Sequence 26 Application PC/TUS9512401A
Sequence 26 Application:
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: TASSET, DIANE
TITLE OF INVENTION: HIGH-AFPINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO IMMUNGLOBIN E
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
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8400 East Prentice Avenue, Suite 200
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
MEDIUM TYPE: storage
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1 Similarity 76.7%; Pred. No. 19;
23; Conservative 0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX23C/PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
FILING DATE: 27 SEPTEMBER 1995
                                                                                                                                                                                                                                                                                                                                                                                        6 ttcaatctgctcatgcattacccaccccc 35
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APPLICATION NUMBER: 08/471,985
FLING DATE: 06-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/317,403
FLING DATE: 03-OCTOBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILNG DATE: 10-JUNE-1991
PRIOR APPLICATION NUMBER: 07/734,428
APPLICATION NUMBER: 07/736,428
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TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 26:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
                                                            TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                ;
OTHER INFORMATION:
US-08-471-985A-28
                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Englewood STATE: Colorado COUNTRY: IIS?
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage COMPUTER: 1BM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,985A
FILING DATE: 06-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-08-411-985A-28/C
Sequence 28, Application US/08471985A
Sequence 28, Application US/08471985A
Sequence 28, Application US/08471985A
Setent No. 568592
GENERAL INFORMATION:
APPLICANT: WIEGAND, Torsten Walter
APPLICANT: WIEGAND, Larry
APPLICANT: TASSET, Diane
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS TO
TITLE OF INVENTION: IMMUNOGLOBIN E
                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S: Swanson & Bratschun, L.L.C.
8400 East Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: All U's are 2'-NH2 uracil
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.7%; Score 18.8; E
Best Local Similarity 76.7%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICATION DATE: 07/714,131
PRIOR DATE: 10-JUNE-1991
PRIOR APPLICATION DATE: 07/536,428
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: BAIRY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX23/CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1993-3333
         NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFRENCE/DOCKET NUMBER: NEX23/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/317,403
FILING DATE: 03-00TOBER-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson &
                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 8400 Eas
CITY: Englewood
STATE: Colorado
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Sequence 2, Application PC/TUS9513536
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SYNTHESIS OF METHYLASE RESISTANT GENES
NUMBER OF SEQUENCES:
CORRESPONDENCE ANDRESS:
ANDRESSEE: BILLIOTT KORSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 239;
                                                                                                                           Length 91;
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                  FEATURE: OTHER INFORMATION: All C's are 2'-NH2 cytosine
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                                                           All U's are 2'-NH2 uracil
                                                                                                                                 DB
                                                                                                                             ; Score 18.8; DE; pred. No. 19; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.1%; Score 18.6; I
Best Local Similarity 72.7%; Pred. No. 28;
Matches 24; Conservative 0; Mismatches
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13-0CT-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                 Query Match 53.7%;
Best Local Similarity 76.7%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KORSEN, ELLIOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-09-437-457-17
                                                             CT-US95-12401A-28
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MOLECULE TYPE:
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LENGTH: 239
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                                                                                           All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                            RESULT 7
PCT-0595-12401A-28/C
Sequence 28, Application PC/TUS9512401A
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: TO IMMUNGLOBIN E
NUMBER OF SEQUENCES: 112
CORRESONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite 200
                                                                                                                               All U's are 2'-NH2 uracil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
MEDIUM TYPE: Storage
COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: WordPeriect 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                              53.7%; Score 18.8; D
76.7%; Pred. No. 19;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US95/12401A
FILING DATE: 27 SEPTEMBER 1995
                                                                                                                                                                                                                                                                                      47 TTCACTCTGTTCACTCATTATCCGCCCCAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEX23C/PCT
                                                                                                                                                                                                                                                                     6 ttcaatctgctcatgcattacccaccccc 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,985
FILING DATE: 06-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/317,403
FILING DATE: 03-OCTOBER-1994
PRIOR APPLICATION DATA: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA: 1991
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: NETELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    Query Match 53.7%
Best Local Similarity 76.7%
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
                                                                                                                                 OTHER INFORMATION:
                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Englewood STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80111
                                                                                                                                                   PCT-US95-12401A-26
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Replan, Jerry
APPLICANT: Peron, Charles
APPLICANT: Moore, Karen
TITLE OF INVENTION: COMPOSITIONS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
NUMBER OF SEQUENCES:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.1%; Score 18.6; DB 4; Length 3552; 72.7%; Pred. No. 49;
                                                                                                                                                                                               APPLICANT: Telford, David L.
APPLICANT: Telford, David L.
APPLICANT: Cutting, John A.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF FELINE
TITLE OF INVENTION: INFECTIOUS ANEMIA
FILE REFERENCE: SYNBIO.1008
CURRENT APPLICATION NUMBER: US/09/157,210B
CURRENT APPLICATION NUMBER: 06/059,551
EARLIER PTLING DATE: 1998-09-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 3552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,445
FILING DATE: 21 "MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
        1 ccgccttcaatctgctcatgcattacccaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; LOCATION: (1)...(3552)
; OTHER INFORMATION: n = A, T, C or G
US-09-157-210-3
                                                                                                                                         Sequence 3, Application US/09157210B Patent No. 6204003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08822445 Patent No. 5952223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Haemobartonella Felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 72.73
Matches 24; Conservative
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ZIP: 10036/2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                              US-09-157-210-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-822-445-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SKOPEK, THOMAS R
TITLE OF INVENTION: SYNTHESIS OF METHYLASE RESISTANT GENES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREE: ELLIOTT KORSEN
STREET: 126 E. Lincoln Avenue, P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: US
ZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.6; DB pred. No. 39; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 CCACCTCCAGTCTGGCCCTGCATGCCCCATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 cegeetteaatetgeteatgeattacecaecec 33
                                                                                                                                                                                                                                                                                                                                                     53.1%; Score 18.6; 72.7%; Pred. No. 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/13536
FILING DATE: 13-OCT-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: KORSEN, ELLIOTT
REGISTRATION NUMBER: 32,705
REFERENCE/DOCKET NUMBER: 19257Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4420
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
REGISTRATION NUMBER: 32,705
REFERENCE/DOCKET NUMBER: 19257Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5493
TELEFAX: (908) 594-4720
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9513536
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 53.1%;
Best Local Similarity 72.7%;
Matches 24; Conservative
                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                       Ouery Match 53.1'
Best Local Similarity 72.7'
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     internal
                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
pCT-US95-13536-2
                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                     TOPOLOGY: linear
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Southan, Christopher TITLE OF INVENTION: HUMAN SERINE PROTEASE NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS:
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.4%; Score 18; 70.6%; Pred. No. 7
                                                                     1224 TCCATCTGCTCTTTCCATACCGACCCCC 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
                                                                                                                                                                                  Sequence 13, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Livi, George
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michel
                                          7 teaatetgeteatgeattaccaccec 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-448-194-3/c ; Sequence 3, Application US/08448194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGEWT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P505
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.4
Best Local Similarity 70.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 610-270-50 TELEFAX: 610-270-5090
        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
, ORIGINAL SOURCE:
US-08-923-454A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19406
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                                                                                                                                                        RESULT 14
US-08-923-454A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: PA
        22;
             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 6830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JOSEPH, Rajiv
APPLICANT: JOSEPH, Rajiv
APPLICANT: Dou, Dexian
TITLE OF INVENTION: A NOVEL NEURONAL-NEONATAL GENE:
TITLE OF INVENTION: NERRONATIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADRRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5837535thwestern Hwy.
CITY: Parmington Hills
STATE: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.4;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  53.1%; Score 18.6;
84.0%; Pred. No. 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 1059.
TELECOMMUNICATION INFORMATION:
TELEFRAX: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08602093
Patent No. 5837535
GENERAL INFORMATION:
                    REFERENCE/DOCKET NUMBER: 7853
TELECOMUNINCATION INFORMATION:
TELEPRONE: 212-790-9090
TELEFAX: 212-869-8864
TELEFAX: 212-869-8864
TELEFAX: 6141 FENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6830 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence
LOCATION: 1...6558
OTHER INFORMATION:
US-08-822-445-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3973 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.1%
Best Local Similarity 84.0%
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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CREMEAL INCOMATION.

CREMEAL INCOMATION.

PAPLICANT: LOSGAN, Michoel

APPLICANT: CANONS, Michoel

APPLICANT: CANONS, Michoel

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APPLICANT: SCHWENT, MAINTENN, Bernadette

APPLICANT: SCHWENT, MAINTENN, MICHOEN

TITLE OF INVESTION: BAF KARAGERTS CORING COR HE TRANSFERSIN

TITLE OF INVESTION: REPERPOR OF BEISSERIA MENNITIDIS

CONSTRESS: P.O. BOX 1404

STREET: P.O. BOX 1404

STREET: P.O. BOX 1404

CONFILES: MAINTENNE CRNH.

CONFILES: MAINTENNE CRNH.

MAINTENNE ELDOR MISSERIA

CONFILES: MAINTENNE CRNH.

MODINATION DATE: STANSFERSIN

CONFILES: MAINTENNE CRNH.

MAINTENNE MAINTENNE STANSFERSIN

CONFILES: MAINTENNE CRNH.

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APPLICANTION NUMBER: US GOOTS AND STANSFERSIN

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APPLICANTION NUMBER: WE SOOTS AND STANSFERSIN

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APPLICANTION NUMBER
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Search completed: February 20, 2002, 14:32:31 Job time: 14410 sec

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Eukaryota Supreus

Eukaryota Sutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201)

1 (bases 1 to 201)

1 (bases 1 to 201)

2 (agria Correa R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Nagai,M.A., deoliveira,P.S., Bucher,P., Jongeneel,G.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Sinpson,A.J.

Sinpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. Twis entry can be seen in the following URL
Oglo00-021-010643-2000-10-0944-1)
Seq primer: puc 18 forward
AU031552 AU031552
BF52144 EST458890
AL064726 Drosophil
AZ578207 20a06 Sho
A0121606 HS, 3079 B
BR284178 601099471
BH007554 ee68H07, x
BE73309 601573220
AT131784 uc37a06, x
BE733197 BB033197
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BE73287 WHE0016_H
AW181048 MgA0545r
BE742877 WHE0016_H
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RC6-CI0122-091000-021-D10 CI0122 Homo sapiens CDNA, mRNA sequence.
BF799331 GI:12128320
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Hommons sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 273)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

R.S. Adams, M.D., Earle-Hughes, J., Findon, E.C., Clayton, R.A.,

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White,

C.J., Lee, N.H., Kirkness, E.F., Meinstock, R.G., Gocayne, J.D., White,

C.J., Lee, N.H., Kirkness, E.F., Meinstock, R.C., Clayton, R.A.,

C.J., Lee, N.H., Kirkness, E.F., Meinston, S.G., Colayne, J.D., Fitzgerald

J.L., Fitzhquy, W.M., Fritchman, J.L., Gocaphagen, N.S., Glodek, A.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Rhillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Bednarik, D.P., Green, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, I.,

Weily, S., Green, J.M., Gruber, J., Hudson, P., Kim, A.K., Raymond, I.,

Weily, R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and

Weiter, B. Weiler, B. Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi/hdi).
Seq primer: M3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1...273 /-
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/db_xref="taxon:9606"
/cb_laxpe="T-14xon:9606"
/cell_Lype="T-14xoncyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA311787 273 bp mRNA EST 19-APR-1997 EST182503 Jurkat T cells VI Homo sapiens CDNA 5' end similar to similar to T-cell factor 1, A/B/C, mRNA sequence.
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                               Ouery Match
Best Local Similarity 100.0%; Score 35; DB 11; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 35; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 0.052;
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 others
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Matches 33; Conservative
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AUTHORS
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S NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) (Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC

CONA Library Preparation: Ling Hong/Rubin Laboratory CONA Library Arrayed by: The I. M.A.G.E. Consortium (IJ.NL)

DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL, at: http://image.llnl.gov h column: 02 High quality sequence stop: 276.

Location/Qualifiers
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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602455204F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4583473
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_15"
High quality sequence start: 16
High quality sequence stop: 201.
Location/Qualifiers
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Fax: 01-40-200-3410

Email: genome-resegscriken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.pv. Nishiyama.Yr. Westover.A., Itoh,M., Nagaoka,S., Sasaki
URL:http://genome.gsc.riken.go.jp/
Carninci.pv. Nishiyama.Yr. Westover.A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis so f full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
Dlasse vieit our web site, Whith Alloyd
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further details.
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ccgccttcaatctgctcatgcattacccaccccc 35
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/dev_stage="adult"
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/strain="C57BL/6J"
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/clone="9230105F22"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1 (bases 1 to 400)
1 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hiller, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Hiller, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Jackson, Y. and Bowers, Y. (cole, R., Tsagareishvili, R., Williams, T.,
Jackson, Y. and Bowers, Y. (stagareishvili, R., Williams, T.,
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
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AA958693/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI: Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference (for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: Life 3 NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
  oligo-dT priming. XhoI site destroyed during cloning. Size-selected by column fractionation, average insert size 1.2kb. Primary library, unamplified."

1.48 c 98 g 67 t
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                                                                                                                                                                                                                                                                                                                                         BI154476 649 bp mRNA EST 05-JUL-2001
602904810F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5034194 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Euteleostomis, Muscului, Muridae, Murinae, Mus.

1 (bases 1 to 649)

NH HWG Chttp://mgc.nci.nih.gov/.

NAtional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLAMI1095 row: d column: 03

High quality sequence stop: 647.
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Pred. No. 7.1;
                                                                                                                                     Length 400;
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/db_xref="taxon:10090"
/clone="InAMGE:5034194"
/tissue_type="tumor, gross tissue"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                 Score 27; DB 11;
Pred. No. 6.9;
0; Mismatches 5;
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ilarity 85.7%;
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Matches 30; Conservative
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BI154476
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IMAGE:1344933 5' similar to gb:X59869 TRANSCRIPTION FACTOR-7 (HUMAN); gb:X61385 Mouse mRNA for T-cell specific transcription factor
AIO49127 288 bp mRNA EST 08-JUL-1998 ub35d04-11 Soares_thymus_ZNDMT Mus musculus cDNA clone IMAGE:1379719 5' similar to qb:X59869 TRANSCRIPTION FACTOR-7 (HUMAN ); qb:X61385 Mouse mRNA for T-cell specific transcription factor (MoUSE);, mRNA sequence.
                                                                                                                                                                                                                                              Mus musculus
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 288)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Lacy,M., Marrin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lacy,M., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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/sex="male"
/tissue_type="Thymus"
/dew_stage="1 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
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llarity 90.3%; Pred. No. 13;
Conservative 0; Mismatches
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/strain="C57BL/6J"
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/clone="IMAGE:1379719"
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AA958693
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AL Onder http://mgc.nci.nih.gov/.

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLAM9524 row: j column: 21

High quality sequence stop: 587.

S Location/Qualifiers

lrce / Organism="Mus musculus"

/ Strain="FVB/N"

/ Ab_xref="taxon:10090"

/ Clone="Index: 193012"

/ Clone="Index: 19100"

/ Average insert size 1.3 kb. Constructed by Life

Technologies. Note: this is a NC1_CGAP Library."

146 a 194 C 136 C 136 C 166 C 136 C 136 C 166 C 136 C 136 C 136 C 166 C 136 C 136 C 136 C 166 C 136 
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C9"
/db_xref="taxon:3055"
/clone="CM023b12_r"
/clone="CM023b12_r"
/clone_lib="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/dev_stage="Vector: pBluescript1[ SK-; Site_1: EcoRl; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydomonas reinhardtii.
Chlamydomonas rcinhardtii
Eukaryota, Viridiplantae; Chlorophyta, Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV387748 516 bp mRNA EST 29-SEP-2000 AV387748 Chlamydomonas reinhardtii c9 Chlamydomonas reinhardtii cDNA clone CM023b12_r, mRNA sequence.
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Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S.
A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundunt expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
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    516
/organism="Chlamydomonas reinhardtii"

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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 cogeetteaatelgeteatgeattaceace (31/
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 587)
                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="iMAGE:1344933"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 CTGCCTTCAATCTGCTCATGCCCTACCCACC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 167
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
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                               AA958693.1 GI:3124923
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BF538482
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Oryza sativa.
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BF279037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         // sex="male" // dev_stage="newly eclosed adults and pharate adults" // dev_stage="newly eclosed adults and bharate adults" // dev_host="%xii Blue MRF and SOLR" // ini-ZAP XR; Site_1: EcoRI; Site_2: XhoI; The library was prepared by Stratagene using oligo-T priming and unidirectional cloning with an adaptor at the 5' end (GCACGAC) following the EcoRI site. The mRNA was prepared from antennae of late pupal and newly eclosed male moths. Clones were subcloned in vivo in mass into pluescript maintained in SOLR cells for DNA sequencing."
                                                                                                                                                                                                                      AI234477 465 bp mRNA EST 02-OCT-2000 EST380 Manduca sexta male antennae Uni-ZAP XR library Manduca sexta debyodrogenase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            Manduca sexta
Manduca sexta
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea; Sphingidae; Sphinginae; Manduca.
1 (bases 1 to 465)
Robertson,H.M., Martos,R., Sears,C., Todres,E.Z., Walden,K.O.
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Diversity of odourant binding proteins revealed by an expressed Sequence tag project on male Manduca sexta moth antennae Insect Mol. Biol. 8, 501-518 (1999)
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/organism="Manduca sexta"
/db xref="taxon:1130"
/clone="pMsmaD135"
/clone="pMsmaD135"
/clone="pMsmaD135"
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                                                                 Length 516;
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                                                                                                    Indels
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Department of Entomology
University of Illinois at Urbana-Champaign
505 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 333-0489
Fax: 217 244 3499
                                                               Score 22.4; DB 10;
Pred. No. 2.9e+02;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.4%; Score 22.2; DB 10;
77.1%; Pred. No. 3.4e+02;
Live 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hughrobe@uiuc.edu
Insert Length: 1500 Std Error: 0.00
Seq primer: T3
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78
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Location/Qualifiers
 164
                                                                                                                                                                                                                                                                                                                                           AI234477.1 GI:3827995
                                                                   64.0%;
81.2%;
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Best Local Similarity 77.19
Matches 27; Conservative
 Ö
                                                                                 Best_Local Similarity 81.29
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                               tobacco hornworm.
 157
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 117
                                                                      Query Match
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Gossypium arboreum.

Gossypium arboreum.

Gossypium arboreum.

Gossypium arboreum.

Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;

Rosidae: eurosids II: Malvales: Malvaceae: Gossypium.

E. I (bases I to 701)

Wing, R.A., Frisch, D., Yu.Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

Unpublished (2000)

Contact: Wing RA

Contact: Wing RA

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293
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1 (bases 1 to 558)
Sasaki, T. and Yamamoto, K.

Frice CDNA from immature leaf including apical meristem (uppublished (1997)
BF279037 701 bp mRNA EST 07-MAR-2001
GA_BD0036M14f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_BD0036M14f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="ARA"
/cultivar="8400"
/db_xref="taxno:29729"
/clone="64_EB0036M14f"
/clone=lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU031552 558 bp mRNA EST 30-OCT-1998 AU031552 Rice cDNA from immature leaf including apical meristem oryza sativa cDNA clone E61840_1A, mRNA sequence.
AU031552.1 G1:3767442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. col!"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
175 c 112 g 207 t 18 others
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Pred. No. 4.9e+02;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gossypium arboreum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Seq primer: TRATACGACTACTATAGGG
High quality sequence step: 698.
High quality sequence stop: 698.
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1. .701
                                                                                                       BF279037
BF279037.1 GI:11210107
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78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 62.3'
Best Local Similarity 78.8'
Matches 26; Conservative
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0

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8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-: Site_1: EcoRI; Site_2:
Xhoi; cNNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifolii. The cDNA was
directionally 1 ligated into the Uni-ZAP RN vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells. Note: EST may
be of fungal origin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buifalo.

NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Prosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP from and how to order Individual BAC clones, the entire library and how to order Individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://dacation from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanoyaster denome survey sequence T7 end of BAC # BACR08L15 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Eplydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 970)
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 612;
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/db_xref="texon:7227"
/clone_lib="RPCI '98"
/clone="BACRO8L15"
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Pred. No. 6.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                              Match 61.1%; Score 21.4; DB 11;
Local Similarity 80.6%; Pred. No. 6.7e+02;
Los 25; Conservative 0; Mismatches 6;
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Total (Bases 1 to 612)

Fedorova, M., Plerson, B.L., Samac, D.A., Vance, C.P., Gautt, G.S., Peng, M. P. Elis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.

Ears from leaves of Medicago truncatula after inoculation with Collectrichum trifolii
Unpublished (2000)

Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
Department of Minnesota
1991 Upper Buford Circle, St. Paul, MN 55108, USA Tel: 612 625 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula
bukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M278859e
TidR sequence name: MTPDH38TK
More information is available at: http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTP gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                 /db_xref="txpon:4530"
/clone="E61840_lA"
/clone_lib="Rice cDNA from immature leaf including apical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="cotyledons and primary leaves harvested 5 and
                        National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondal 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                  Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF521414 612 bp mRNA EST U8-DEC-2000
EST458890 DSIL Medicago truncatula cDNA clone pDSIL-43G4, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="immature"
/note="Organ: leaf; immature leaf including apical
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/tissue_type="leaves infected with ColletoLrichum
trifolii"
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120 c 162 g 147 t 2 ot
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Pred. No. 6.7e+02;
0; Mismatches 6;
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/cultivar="genociype A17"
/db.xref="taxon:3880"
/clone="pDSIL-43G4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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/strain="Nipponbare"
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BF521414.1 GI:11610097
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il Similarity 80.6%;
25; Conservative
                                                                              305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
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6; Indels 0; Gaps
31
0; Mismatches
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25; Cor cegecticas
Matches Dy 1 c